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QY      * 121 LTKDKIPLINQLMWA 136
Db      121 LTKDKIPLINQLMWA 136

RESULT 2
Q9MBY4  PRELIMINARY; PRT; 142 AA.
AC      Q9MBY4
DT      31-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Putative response regulator protein (receiver component).
GN      T6K12.10.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Columbia;
RA      Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA      Rowning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA      Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT      "Arabidopsis thaliana chromosome III BAC T6K12 genomic sequence.";
RL      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Haas B.J., Volfovsky N., Town C.D., Trukhan M., Alexandrov N.,
RA      Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT      "Full-length messenger RNA sequences greatly improve genome
RT      annotation.";
RL      Genome Biol. 0:0-0(2002).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA      Feldmann K.;
RT      "Full-length cDNA from Arabidopsis thaliana.";
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AC016829; AAF26786.1; -
DR      EMBL; AY085638; AAM62859.1; -
DR      InterPro; IPR001789; Response reg.
DR      Pfam; PF00072; Response reg; 1.
DR      ProDom; PD000039; Response reg; 1.
DR      PROSITE; PSS0110; RESPONSE_REGULATORY; 1.
KW      Phosphorylation; Sensory transduction.
SQ      SEQUENCE 142 AA; 15792 MW; 57487135FFD5238 CRC64;

Query Match 79.4%; Score 538; DB 10; Length 142;
Best Local Similarity 78.9%; Pred. No. 9.8e-40;
Matches 112; Conservative 8; Mismatches 16; Indels 6; Gaps 2;

QY      1 MATKSMGDIK-----IKKKL-NVLIYDDPLNLIHKIKIAGISQTANGGEAVII 54
Db      1 MATKSTGGTETKSIKVKKKLNVLIVDDPLNRLHEMIITIGISQTAKNGEAVIL 60

QY      55 HRDGGSPDLTMDKPERDGVSTTKKLEMEVKSMIVGVTSIADNEERRAFMEAGNL 114
Db      61 HRDGEAPDLTMDKXENPERDGVSTTKKLEMKVTSWIVGVTSVADQEEERKAFMEAGNL 120

QY      115 HCLAKPLTKDKIPLINQLMWA 136
Db      121 HCLEKPLTKAKIFPLISHLEFDA 142

RESULT 3
Q15763  PRELIMINARY; PRT; 1969 AA.
AC      Q15763
DT      01-JAN-1998 (TREMBlrel. 05, Created)
DT      01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT      01-JAN-1998 (TREMBlrel. 05, Last sequence update)

QY      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Two-component hybrid sensor and regulator.
GN      LA3996.
OS      Leptospira interrogans.
OC      Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX      NCBI_TaxID=173;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA      Ren S.;
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AE011554; AAN51193.1; -
KW      Complete proteome.
SQ      SEQUENCE 820 AA; 94325 MW; 3DBE99966794E67D CRC64;

DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Hybrid histidine kinase DHKB.
GN      DHKB.
OC      Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX      NCBI_TaxID=44689;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Kax3;
RX      MEDLINE=98248997; PubMed=9576830;
RT      Zinda M.J., Singleton C.K.;
RT      "The hybrid histidine kinase dhkb regulates spore germination in
RT      Dictyostelium discoideum.";
RL      Dev. Biol. 196:171-183(1998).
DR      EMBL; AF024654; AAB71889.1; -
DR      InterPro; IPR003594; ATPbind_ATPase.
DR      InterPro; IPR004358; Bact_sens_pr_C.
DR      InterPro; IPR003661; His_KinA.
DR      InterPro; IPR005467; His_Kinase.
DR      InterPro; IPR000014; PAS_domain.
DR      InterPro; IPR001789; Response_reg.
DR      Pfam; PF02518; HATPase_C; 1.
DR      Pfam; PF00512; HSKA; 1.
DR      Pfam; PF00072; response_reg; 1.
DR      PRINTS; PR00344; BCTRLSENSOR.
DR      ProDom; PD000039; Response_reg; 1.
DR      SMART; SM00387; HATPase_C; 1.
DR      SMART; SM00388; HSKA; 1.
DR      SMART; SM00091; PAS; 1.
DR      SMART; SM00448; REC; 1.
DR      TIGRFAMs; TIGR00229; sensory_box; 1.
DR      PROSITE; PS0109; HIS_KIN; 1.
DR      PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW      Kinase; Phosphorylation; Sensory transduction.
SQ      SEQUENCE 1969 AA; 219025 MW; 8E7A7952AB1B552B CRC64;

Query Match 26.7%; Score 181; DB 5; Length 1969;
Best Local Similarity 35.8%; Pred. No. 5.1e-07;
Matches 48; Conservative 29; Mismatches 39; Indels 18; Gaps 5;

QY      10 EIKKKLVLIYDDPLNLIHKIKIAGISQTANGGEAVIIHRDGGSPDLILMDX 69
Db      1836 EKIEK--ILLVEDNFVNKIFSKLLKDSGYIFDVAHNGVEAVCEVKKG--AYDLILMD 1890

QY      70 EMPERDGVSTTKKLEMEVKSMI-----VGVTSLADNE--ERRAFMEAGLNHCL 117
Db      1891 QMPEDMGFEATTARELEKSNLIESPPSKHSHVIVALTANSYKQKCLSVGMNDEL 1950

QY      118 AKPL-TKDKIPLI 130
Db      1951 QRPKTSILIQMI 1964

RESULT 4
Q8EZ63  PRELIMINARY; PRT; 820 AA.
AC      Q8EZ63;
DT      01-MAR-2003 (TREMBlrel. 23, Created)
DT      01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Two-component hybrid sensor and regulator.
GN      LA3996.
OS      Leptospira interrogans.
OC      Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX      NCBI_TaxID=173;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA      Ren S.;
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AE011554; AAN51193.1; -
KW      Complete proteome.
SQ      SEQUENCE 820 AA; 94325 MW; 3DBE99966794E67D CRC64;

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Query Match      26.5%; Score 179.5; DB 16; Length 820;
Best Local Similarity 31.6%; Pred. No. 2.4e-07;
Matches 43; Conservative 29; Mismatches 49; Indels 15; Gaps 5;

QY 8 DIEK-----IKKLVNLIIVDDPNNLIHEKIIKAIGISQATNNGEAVIIHRDGGSPF 62
DB 679 DLEKSFQDVAKSTRILVAEDNETNCLLIERALKKLGVDPTVHNGRE--VIERMQLEAF 736
QY 63 DLIILDKEMPERDGVSTTKKLEMEVKS--MIVGVTSLADNEERAFMEAGLNHCLAK 119
DB 737 DLIILDIEMPEVDGHEATKWRKNSQNSFEFFIIIALTADA-ISSKKEYISKWNDCLTK 795
QY 120 PLTKDKIPLINQLMD 135
DB 796 PLD----LPILKSTLD 807

RESULT 5
Q8CVU5 PRELIMINARY; PRT; 1197 AA.
AC Q8CVU5;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Sensor protein evgs precursor (EC 2.7.3.-).
GN EVGS OR C2306.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwatz F.R.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AE016764; AA081356.1; -.
KW Transferrase; Complete proteome.
SQ SEQUENCE 1197 AA; 134847 MW; 5088214E7F834F06 CRC64;

Query Match      26.3%; Score 178.5; DB 16; Length 1197;
Best Local Similarity 34.4%; Pred. No. 4.6e-07;
Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;

QY 12 IKKLVNLIIVDDPNNLIHEKIIKAIGISQATNNGEAVIIHRDGGSPFDLIIMDKEM 71
DB 955 LPEKLSILADDPHTNRLILKRLQNLGVDVDEATDGVQA--LHKVSMQHYDLITDVMN 1012
QY 72 PERDGVSTTKKLEMEVKSMTVGTSLADNEERAFMEAGLNHCLAKPLTKDKIIPLIN 131
DB 1013 PNMDSGELTRKLEQNSLPITNGLTANA-QANEREKGLNCGMNLCLPPLTDLVLKTHLS 1071
QY 132 QL 133
DB 1072 QL 1073

RESULT 6
Q9A3P0 PRELIMINARY; PRT; 394 AA.
AC Q9A3P0;
DT 08-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Sensor histidine kinase/response regulator.
GN CC3162.
OS Caulobacter crescentus.

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OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
RX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heideberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA DePocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Iran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
DR EMBL; AE005980; AAK25124.1; -.
DR HSSP; P06857; 2CHP.
DR TIGR; CC3162; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR005467; His_Kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00072; Response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
DR Kinase; Phosphorylation; Sensory transduction; Complete proteome.
SQ SEQUENCE 394 AA; 41592 MW; 6D9AF0B278B70E70 CRC64;

Query Match      25.7%; Score 174; DB 16; Length 394;
Best Local Similarity 31.7%; Pred. No. 3.1e-07;
Matches 39; Conservative 31; Mismatches 49; Indels 4; Gaps 2;

QY 14 KKLNVLIIVDDPNNLIHEKIIKAIGISQATNNGEAVIIHRDGGSPFDLIIMDKEMPE 73
DB 262 RSAHLIVDDNATNMYVAALCDMFECTSEQAVDGVAVEMASG--RFDLIIMDKMPR 319
QY 74 RDGVSTTKKLEMEVKSMTVGTSLADNER--RRAFMEAGLNHCLAKPLTKDKIIPLIN 131
DB 320 MDGVAATRAIRELSGRSSAIPVALTANADPADVHTYLAAGMDQVVEKIPKPERLALVN 379
QY 132 QLM 134
DB 380 SLL 382

RESULT 7
Q8FFP9 PRELIMINARY; PRT; 949 AA.
AC Q8FFP9;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Sensor protein rcsC (EC 2.7.3.-).
GN RCSC OR C2761.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwatz F.R.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence

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RT of uropathogenic Escherichia coli. ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AB016763; AAN81215.1; --
KW Transferase; Complete proteome.
SQ SEQUENCE 949 AA; 106590 MW; DF8CA47F9EEB4088 CRC64;

Query Match 25.6%; Score 173.5; DB 16; Length 949;
Best Local Similarity 33.6%; Pred. No. 9.7e-07;
Matches 37; Conservative 35; Mismatches 33; Indels 5; Gaps 3;

QY 18 VLIVDDPPLNLIHKKIKAIGISQTNNGEEAVIHRDGGSSFDLILMDKEMPERDG 76
Db 827 ILVDDHPINRLLADQLGSLGYCKTANGVDALNVLK---NHIDIVLSDVNMVNDG 883
QY 77 VSTTKLREMEVKSMIVGTVSLADNEERRAFMEAGLNHCLAKPLTKDKI 126
Db 884 YRLTQRIQRLGLTLPVIGVTANALAEKQRC-LESGMDSCLSKPVTLDVI 932

RESULT 8
Q9RLC7 ID Q8X339 PRELIMINARY; PRT; 417 AA.
AC Q8X339;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative histidine kinase (fragment).
GN GACS.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JN300;
RA Graupner S., Wackernagel W.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ249741; CAB56474.1; --
DR InterPro; IPR002570; Hpt.
DR InterPro; IPR001789; Response reg.
DR Pfam; PF00072; response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00073; HPT; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS01110; RESPONSE REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
FT NON TER 1 1
SQ SEQUENCE 417 AA; 45749 MW; D196B4FFDDA23BB2 CRC64;

Query Match 25.5%; Score 173; DB 2; Length 417;
Best Local Similarity 32.8%; Pred. No. 4e-07;
Matches 39; Conservative 35; Mismatches 37; Indels 8; Gaps 3;

QY 17 NVLIVDDPPLNLIHKKIKAIGISQTNNGEEAVIHRDGGSSFDLILMDKEMPERDG 76
Db 169 SVLCVDNDPANMLLETLTLDNGEAVVAVSSGQALEVVQQ--QSFDFVFDVQNGMDG 226

QY 77 VSTTKLREMEVKSMIVGTVSLADNEERRAFMEAGLNHCLAKPLTKDKIPLI 130
Db 227 RQTEAIRRELESQGPPLPVALTAHA-LSNERRSLQSLDYLTKPISEBQLAQV 284

RESULT 9
Q8XE39 ID Q8XE39 PRELIMINARY; PRT; 933 AA.
AC Q8XE39;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sensor for ctr capsule biosynthesis, probable histidine kinase
DE acting on RCSC.
GN RCSC OR Z3477 OR ECS3107.
OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIND 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22 (2001).
DR EMBL; AE005454; BAG57353.1; --
DR EMBL; AF002560; BAG36530.1; --
DR HSSP; P06143; ID4Z.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003661; His_kinase.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HisKA; 1.
DR PRINTS; PR00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; HisKA; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS01109; HIS_KIN; 1.
DR PROSITE; PS01110; RESPONSE REGULATORY; 1.
KW Kinase; Complete proteome.
SQ SEQUENCE 933 AA; 104605 MW; 5755C05F713E561D CRC64;

Query Match 25.3%; Score 171.5; DB 16; Length 933;
Best Local Similarity 33.9%; Pred. No. 1.4e-06;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 18 VLIVDDPPLNLIHKKIKAIGISQTNNGEEAVIHRDGGSSFDLILMDKEMPERDG 77
Db 811 ILVDDHPINRLLADQLGSLGYCKTANGVDALNVL--SKNHIDIVLSDVNMVNDG 868

QY 78 STTKLREMEVKSMIVGTVSLADNEERRAFMEAGLNHCLAKPLTKDKI 126
Db 869 RLTIQRIQRLGLTLPVIGVTANALAEKQRC-LESGMDSCLSKPVTLDVI 916

RESULT 10
Q8ZGR4 ID Q8ZGR4 PRELIMINARY; PRT; 957 AA.
AC Q8ZGR4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two component sensor kinase/response regulator protein Rcsc
DE (EC 2.7.3.-) (Sensor for ctr capsule biosynthesis).
GN RCSC OR YP01217 OR Y2971.
OS Yersinia pestis.

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JC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
JC Enterobacteriaceae; Yersinia.
JC NCBi_TaxID=632;
JC [1]
JC SEQUENCE FROM N.A.
JC STRAIN=CO-92 / Biovar Orientalis;
JC MEDLINE=21470413; PubMed=11586360;
JC A Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
JC A Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
JC A Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
JC A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
JC A Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
JC A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
JC A Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
JC "Genome sequence of Yersinia pestis, the causative agent of plague."
JC Nature 413:523-527(2001).
JC [2]
JC SEQUENCE FROM N.A.
JC STRAIN=KIM5 / Biovar Mediaevalis;
JC MEDLINE=22137863; PubMed=12142430;
JC Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
JC A Peria N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
JC A Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
JC A Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
JC A Perry R.D.;
JC "Genome sequence of Yersinia pestis KIM."
JC J. Bacteriol. 184:4601-4611(2002).
JC EMBL; AJ414147; CAC90055.1; -.
JC EMBL; AE013898; AAM86522.1; -.
JC HSP; P06143; I04Z.
JC InterPro; IPR003594; ATPbind_ATPase.
JC InterPro; IPR004358; Bact_sens_pr_C.
JC InterPro; IPR003661; His_KinA.
JC InterPro; IPR005467; His_kinase.
JC InterPro; IPR001789; Response_reg.
JC Pfam; PF02518; HATPase_C; 1.
JC Pfam; PF00512; HSKA; 1.
JC Pfam; PF00072; response_reg; 1.
JC PRINTS; PR00344; BCTRLSENSOR.
JC ProDom; PD000039; Response_reg; 1.
JC PROSITE; PS50109; HIS_KIN; 1.
JC PROSITE; PS50110; RESPONSE_REGULATORY; 1.
JC Kinase; Transferase; Complete proteome.
JC SEQUENCE 957 AA; 108591 MW; 0447A11F59100011 CRC64;

Query Match 25.3%; Score 171.5; DB 16; Length 957;
Best Local Similarity 35.1%; Pred. No. 1.5e-06;
Matches 39; Conservative 29; Mismatches 40; Indels 3; Gaps 2;

2Y 16 LNVLIYDDPLNLIHEKIIKAGISQATNNGEAEVLIHRDGGSSFDLILMDKEMPERD 75
Db 835 LQILVVDHPINRLLADQLTTLGVRVITANDGLDALVNT--NTVDVLTVDVNPND 892

2Y 76 GVSTTKKLRMEVKSIMVGVTSIADNEERRAFMEAGLNHCLAKPLTKDKI 126
Db 893 GYRLTERLQLNHNFPPIIGVTANALAEKQRC-IEAGMDNCLSKPVTDLTL 942

RESULT 11
ID Q9ANYO PRELIMINARY; PRT; 927 AA.
AC Q9ANYO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Two-component system sensor protein.
DE RSCS.
GN RSCS.
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBi_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=21142508; PubMed=11208780;
RX Visick K.L., Skoufos L.M.;
RX "A two-component sensor required for normal symbiotic colonization of
RX Euprymna scolopes by Vibrio fischeri.";
RX J. Bacteriol. 183:835-842(2001).
RX CC -1- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
RX KINASES.
DR EMBL; AE319618; AAG60694.1; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003661; His_KinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR002570; Hpt.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000044; PAS_domain.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HSKA; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; HSKA; 1.
DR SMART; SM00073; HPT; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00448; REC; 1.
DR TIGRFAWS; TIGR00229; sensory_box; 1.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50113; PAC; 1.
DR PROSITE; PS50112; PAS; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
DR Kinase; Phosphorylation; Sensory transduction; Transferase.
KW SEQUENCE 927 AA; 105590 MW; 9EE0659CB2E8BFB8 CRC64;

Query Match 25.2%; Score 171; DB 2; Length 927;
Best Local Similarity 33.9%; Pred. No. 1.6e-06;
Matches 43; Conservative 28; Mismatches 42; Indels 14; Gaps 4;

QY 16 LNVLIYDDPLNLIHEKIIKAGISQATNNGEAEVLIHRDGGSSFDLILMDKEMPERD 75
Db 659 LSLIIAEDNKNALVAQMFQCRIGHKAIIEAGK--VAIDKIKETHFDLIINDNEMPND 716

QY 76 GVSTTKKLRMEVKSIMVGVTSIADNEERRAFMEAGLNHCLAKPLTKDKI 129
Db 717 GILATKIIRKLIKISTVIFAYTANAFQKADN-----FLKAGANYVLTPLQENDFICA 770

QY 130 INQLMDA 136
Db 771 IKQYQDA 777

RESULT 12
ID Q8FQ37 PRELIMINARY; PRT; 769 AA.
AC Q8FQ37;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two-component system sensor protein.
DE XAC0494.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBi_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RC MEDLINE=22022145; PubMed=12024217;
RX

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Query	Match	Score	DB	Length	Indels	Gaps
QY	17	NVLIVDDDPNLIIHKKIKATGGISQTANNEBAVITHRDGSGSFDLIIIMDKEMPERDG	76			
DB	1033	HLLVVDSINCEVAORILEGEGAMVTVAHDGEQAVSTLKRAPNLFHLVLMVDQMPVVDG	1092			
QY	77	VSTTKLREMEVKSM--IVGVTSLSADNEERAEAFMEAGLNCHLAKPLTKDKIIPLINQLM	134			
DB	1093	YEATRLRQIPALASLPVIALTAGAPFPQEXA-LEAGMNGFIKAFNFVVELTAIRHFL	1151			
RESULT 14						
085663		PRELIMINARY;	PRT;	507	AA.	
ID	085663					
AC	085663;					
DT	01-NOV-1998 (TrEMBLrel. 08, Created)					
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)					
DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)					
DE	RCSC (Fragment).					
GN	RCSC.					
OS	Proteus mirabilis.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;					
OC	Enterobacteriaceae; Proteus.					
OX	NCBI TaxID=594;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-BB2000;					
RX	MEDLINE=98047557; PubMed=9829920;					
RA	Belas R., Schneider R., Meich M.;					
RT	"Characterization of Proteus mirabilis precocious swarming mutants: identification of tsbA, encoding a regulator of swarming behavior."					

```

J. Bacteriol. 180:6126-6139(1998).
-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
KINASES.
DR EMBL; AF071215; AAC82662.1; -.
DR HSSP; P06657; 2CHF.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction; Transferase.
FT NON_TER 1
SQ SEQUENCE 507 AA; 57326 MW; F5DA2EAD9C35DEFS CRC64;

Query Match 24.6%; Score 166.5; DB 2; Length 507;
Best Local Similarity 36.4%; Pred. No. 1.9e-06;
Matches 39; Conservative 26; Mismatches 39; Indels 3; Gaps 2;

QY 16 LNVLIYDDPDLNLIHKEIKIIGISOTANGBEAVIHRDGGSSFDLIIMDKEMPERDGV 75
DB 397 LTVLIYDDHPINRLTLTQLKKIGENTATBEDGCDALAFMQE--NHVDIILTVDNFMN 454
QY 76 GVSTTKKREMEVKSIMVGVTSIADNEERRAFNEAGLNHCLAKPLT 122
DB 455 GYQLATTVELSSTPIIGVTANATAEKKQRC-IDAGMNDVCVKPVS 500

RESULT 15
ID Q8P883 PRELIMINARY; PRT; 1364 AA.
AC Q8P883;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-NAR-2003 (TRENBLrel. 23, Last annotation update)
DE Two-component system sensor protein.
GN XCC2360.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Gicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Kocai E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012344; AAM41638.1; -.

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DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR002570; Hpt.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-associ_C.
DR InterPro; IPR000114; PAS_domain.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF00785; PAC; 2.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF00072; response_reg; 2.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 2.
DR TIGRFAMS; TIGR00229; sensory_box; 2.
DR PROSITE; PS50839; CHASE; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50113; PAC; 2.
DR PROSITE; PS50112; PAS; 2.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 2.
KW Complete proteome.
SQ SEQUENCE 1364 AA; 150167 MW; 48F1C5FBD9710316 CRC64;

Query Match 24.1%; Score 163.5; DB 16; Length 1364;
Best Local Similarity 30.3%; Pred. No. 1.1e-05;
Matches 36; Conservative 36; Mismatches 44; Indels 3; Gaps 3;

QY 18 VLIYDDPDLNLIHKEIKIIGISOTANGBEAVIHRDGGSSFDLIIMDKEMPERDGV 77
DB 1034 LLLYDDSEINCEVAQRILEGEGAMVTVAHDGEQAVNTLKRAPDLFHLVLMVQMPVVDGY 1093
QY 78 STTKKLEEM-EVKSM-IVGVTSIADNEERRAFNEAGLNHCLAKPLTKKIPLINQLM 134
DB 1094 EATRRLRQIPSLASLPVIALTAGAFRPOEKA-LEAGMNGFIAPKPNVELVTAIRHFL 1151

Search completed: August 14, 2003, 16:49:03
Job time : 98 secs

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GenCore version 5.1.6
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WM protein - protein search, using sw model

run on: August 14, 2003, 16:46:47 ; Search time 23 Seconds
(without alignments)
278.071 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678

Sequence: 1 MATKSMGDIKIKKLNLI.....LAKPLTKXIIPLINQLMDA 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178.5	26.3	1197	1 EVGS_ECOLI	P30855 escherichia
2	176.5	26.0	1197	1 EVGS_ECOLI	P58402 escherichia
3	173.5	25.6	948	1 RCSC_SALTI	Q56128 salmonella
4	172.5	25.4	948	1 RCSC_SALTI	P58662 salmonella
5	171.5	25.3	949	1 RCSC_ECOLI	P14376 escherichia
6	156.5	23.1	777	1 PRZE_WYXA	P18759 myxococcus
7	150	22.1	622	1 SKN1_YEAST	P38889 saccharomyc
8	149.5	22.1	778	1 ARCB_ECOLI	P58383 escherichia
9	149.5	22.1	778	1 ARCB_ECOLI	P22783 escherichia
10	145	21.4	1220	1 SLN1_YEAST	P39928 saccharomyc
11	143.5	21.2	712	1 SKN1_YEAST	Q70084 saccharomyc
12	142	20.9	907	1 GACS_PSESY	P48027 pseudomonas
13	140.5	20.7	226	1 DCTR_BACSU	P56602 bacillus su
14	140.5	20.7	230	1 DCTR_BACSU	Q96988 bacillus ha
15	134	19.8	119	1 CHYR_BACSU	P44072 bacillus su
16	134	19.8	1238	1 EVGS_BORPE	P16575 bordetella
17	133.5	19.7	228	1 DCTR_BACME	P39486 bacillus me
18	133.5	19.7	918	1 BARA_ECOLI	P26607 escherichia
19	132.5	19.5	131	1 YSO1_PLEBO	P51586 plectonema
20	132.5	19.5	859	1 BAZA_SHIFL	P59342 shigella fl
21	132	19.5	859	1 LUXQ_VIBHA	P54302 vibrio harv
22	131.5	19.4	441	1 ZRAR_SALTI	Q82333 salmonella
23	131.5	19.4	441	1 ZRAR_SALTI	P58582 salmonella
24	130	19.2	1238	1 EVGS_BORPA	P40330 bordetella
25	128.5	19.0	849	1 LUXN_VIBHA	P54301 vibrio harv
26	127.5	18.8	522	1 MCS4_SCHPO	P87323 schizosacch
27	127	18.7	1238	1 EVGS_BORBR	P46762 bordetella
28	126.5	18.7	227	1 CPXR_HAEIN	P44895 haemophilus
29	125.5	18.5	443	1 ZRAR_KLEOX	Q9apd9 klebsiella
30	124	18.3	144	1 CHYR_TREPA	P6126 treponema p
31	124	18.3	539	1 PRRI_SCHPO	O14283 schizosacch
32	122.5	18.1	441	1 ZRAR_ECOLI	P14375 escherichia
33	122	18.0	248	1 ALGR_PSEAE	P26275 pseudomonas

RESULT 1					
EVGS_ECOLI					
ID	EVGS_ECOLI	STANDARD;	PRT;	1197	AA.
AC	P30855; P77644; Q9RF36; Q9RF37;				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Sensor protein evgs precursor (EC 2.7.3.-).				
CN	EVGS OR B2370.				
OS	Escherichia coli.				
OC	Bacteria; Proteobacteria; Gammaproteobacteri				
OC	Enterobacteriaceae; Escherichia.				
OX	NCBI_TaxID=562;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12;				
EX	MEDLINE=94171083; PubMed=8125343;				
RA	Utsumi R., Katayama S., Taniguchi M., Horie				
RA	Nakagawa H., Miwa A., Tanabe H., Noda M.;				
RT	"Newly identified genes involved in the sign				
RT	Escherichia coli K-12.";				
RL	Gene 140:73-77(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12;				
EX	MEDLINE=93173621; PubMed=1289796;				
RA	Utsumi R., Katayama S., Ikeda M., Igaki S.,				
RA	Taniguchi M., Noda M.;				
RT	"Cloning and sequence analysis of the evgs				
RT	transduction of Escherichia coli K-12.";				
RL	Nucleic Acids Symp. Ser. 27:149-150(1992).				
RN	[3]				
RP	SEQUENCE FROM N.A. (VARIANTS EVGS1 AND EVGS4).				
RC	STRAIN=K12;				
EX	MEDLINE=20378313; PubMed=10923791;				
RA	Kato A., Ohnishi H., Yamamoto K., Furuta E.,				
RT	"Transcription of emrKY is regulated by the				
RT	system in Escherichia coli K-12.";				
RL	Biosci. Biotechnol. Biochem. 64:1203-1209(20				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12 / MG1655;				
EX	MEDLINE=97426617; PubMed=9278503;				
RA	Blattner F.R., Plunkett G. III, Bloch C.A.,				
RA	Riley M., Collado-Vides J., Glasner J.D., Ro				
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Go				
RA	Mau B., Shao Y.;				
RT	"The complete genome sequence of Escherich				
RL	Science 277:1453-1474(1997).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12;				
EX	MEDLINE=97349980; PubMed=9205837;				
RA	Yamamoto Y., Aiba H., Baba T., Hayashi K.,				
RA	Itoh T., Kimura S., Kitagawa M., Makino K.,				
RA	Mizobuchi K., Mori H., Nakade S., Nakamura				

Q8x613 escherichia
P10957 escherichia
Q34534 bacillus su
Q45994 caulobacter
P16244 escherichia
Q44006 alcaligenes
P49246 xanthomonas
Q56312 thermotoga
P51358 porphyra pu
P43501 pseudomonas
Q06065 escherichia
O78428 guillardia

ALIGNMENTS

FT	DOMAIN	559	1197
FT	DOMAIN	718	938
FT	DOMAIN	960	1074
FT	DOMAIN	1098	1197
FT	MOD RES	721	721
FT	MOD RES	1009	1009
FT	MOD RES	1137	1137
FT	VARIANT	577	577
FT	VARIANT	701	701
FT	CONFLICT	152	152
FT	CONFLICT	242	243
FT	CONFLICT	275	275
FT	CONFLICT	420	421
FT	CONFLICT	739	739
FT	CONFLICT	758	758
FT	CONFLICT	761	761
FT	CONFLICT	877	877
FT	CONFLICT	1045	1045
FT	CONFLICT	1074	1074
FT	SEQUENCE	1197 AA;	134742 MW; 58E1DE0F797B1278 CRC64;
QY	Query Match	26.3%;	Score 178.5; DB 1; Length 1197;
Bst	Local Similarity	34.4%;	Pred.No.2.9e-07;
Matches	42; Conservative	25; Mismatches	52; Indels 3; Gaps 2;
QY	12 IKKLNVLIVDDPDLNLITHEIKIKAIGISOTANNGEEAVIIHRDGGSPDLIMDKEM	71	
DB	955 LPEKSLILADHPTNLLKKQLNLLGYDVDEATGQA--LHKVSNQHYDLLLTIDVM	1012	
QY	72 PERGVSTTKKLREMEVKMIVGTGLANEERAPFMELAGNHCLAKPLPKKIPLIN	131	
DB	1013 PNMGDFLTRKLRQNSSLPINGLTANA-QAVERBKGLSCGMNLCFKPLTLDVLKTHLS	1071	
QY	132 QL 133		
DB	1072 QL 1073		
RESULT 2	EVGS_ECO57		
ID	EVGS ECO57 STANDARD; PRT; 1197 AA.		
AC	P58402;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Sensor protein evgs precursor (EC 2.7.3.-).		
GN	EVGS OR Z3632 OR ECS3249.		
OS	Escherichia coli O157:H7.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
ON	Enterobacteriaceae; Escherichia.		
OX	NCBI_TaxID=83334;		
OR	[1]_TaxID=83334;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=O157:H7 / EDL933 / ATCC 700927;		
RX	MEDLINE=21074935; PubMed=11206551;		
RA	Perna N.T., Plunkett G. III, Burland V., Mau B., Glaesner J.D.,		
RA	Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,		
RA	Fostai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,		
RA	Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,		
RA	Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,		
RA	Welch R.A., Blattner F.R.;		
RT	"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";		
RL	Nature 409:529-533(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=O157:H7 / RMD 0509952;		
RX	MEDLINE=21156231; PubMed=11258796;		
RA	Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,		
RA	Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,		
RA	Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,		
RA	Kuhara S., Shiba T., Hattori M., Shingawa H.,		
RT	"Complete genome sequence of enterohemorrhagic Escherichia coli		
RT	O157:H7 and genomic comparison with a laboratory strain K-12.";		

DN Res. 8:11-22(2001).

CC -!- FUNCTION: Member of the two-component regulatory system evgs/evgA.
 CC Phosphorylates evgA via a four-step phosphorylation in response to
 CC environmental signals (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Probable).

CC -!- PTM: Activation requires a sequential transfer of a phosphate
 CC group from a His in the primary transmitter domain, to an Asp in
 CC the receiver domain and to a His in the secondary transmitter
 CC domain (By similarity).

CC -!- SIMILARITY: Contains 1 histidine kinase domain.

CC -!- SIMILARITY: Contains 1 HPT domain.

CC -!- SIMILARITY: Contains 1 response regulatory domain.

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 CC or send an email to license@isb-sib.ch).

CC -----

EMBL; AE005468; AAG57495.1; -;
 EMBL; AP002561; BAB36672.1; -;
 PIR; A91035; A91035.
 PIR; C85879; C85879.
 InterPro; IPR003594; Atgbind ATPase.
 InterPro; IPR004358; Bact_sens_pr_C.
 InterPro; IPR003461; His_kinA.
 InterPro; IPR005467; His_kinase.
 InterPro; IPR002570; Hpt.
 InterPro; IPR001789; Response_reg.
 InterPro; IPR001311; SBP_glu_receptor.
 InterPro; IPR001638; SBP_bac_3.
 Pfam; PF00518; HiskA; 1.
 Pfam; PF00512; HiskA; 1.
 Pfam; PF00072; response_reg; 1.
 Pfam; PF00497; SBP_bac_3; 1.
 PRINTS; PR00344; BCTRLSENSOR.
 ProDom; PD000039; Response_reg; 1.
 SMART; SM00387; HATPase_c; 1.
 SMART; SM00388; HiskA; 1.
 SMART; SM00073; HPT; 1.
 SMART; SM00062; PBPb; 2.
 SMART; SM00448; REC; 1.
 PROSITE; PS50109; HIS_KIN; 1.
 PROSITE; PS50894; HPT; 1.
 PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 KW Sensory transduction; Transferase; Kinase; Phosphorylation;
 KW Transmembrane; Inner membrane; Signal; Complete proteome.
 FT SIGNAL 1 21
 FT CHAIN 22 1197
 FT DOMAIN 22 325
 FT TRANSMEM 326 346
 FT DOMAIN 347 537
 FT PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 538 558
 FT DOMAIN 559 1197
 FT CYTOPLASMIC (POTENTIAL).
 FT HISTIDINE KINASE
 FT RESPONSE REGULATORY.
 FT DOMAIN 960 1074
 FT HPT.
 FT MOD_RES 721 721
 FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1009 1009
 FT PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1137 1137
 FT PHOSPHORYLATION (BY SIMILARITY).
 SQ -SEQUENCE 1197 AA; 134953 MW; A0105089D9618E2 CRC64;

Query Match 26.0%; Score 176.5; DB 1; Length 1197;
 Best Local Similarity 34.4%; Pred. No. 4.3e-07;
 Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;

CC 12 IKKKLVIVDDPDLNLIIKKAIGISOTANNGEAVIHRDGGSGFDLILMDKEM 71
 CC 955 LPEKLSIIADDPHTNRLLRQLNGLDYDEATDGVQA--LHKVSMQHYDLITDVM 1012

QY 72 PERDGVSTTKLEMEVKSMIVGVTSIADNEERAFMEAGLNHCLAKPLTKDKIIPLIN 131
 DB 1013 PNVDGELTKRQEQNSLPINGLTANA-QANEREKGLNCGWNLCLFPLTLDVLTHTLS 1071
 QY 132 QL 133
 DB 1072 QL 1073

RESULT 3
 RCSC_SALTI STANDARD; PRT; 948 AA.
 ID RCSC_SALTI
 AC Q56128;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Sensor protein rcsc (SC 2.7.3.-) (Capsular synthesis regulator
 DE component C).
 GN RCSC OR STY2496 OR T0594.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham P., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.F., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18";
 RL Nature 413:848-852(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18";
 RL J. Bacteriol. 185:2330-2337(2003).
 RN [3]
 RP SEQUENCE OF 846-948 FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=96198173; PubMed=8626298;
 RA Virlogeux I., Waxin H., Ecobichon C., Lee J.O., Popoff M.Y.;
 RT "Characterization of the rcsA and rcsB genes from Salmonella typhi:
 RT rcsB through tvia is involved in regulation of Vi antigen
 RT synthesis";
 RL J. Bacteriol. 178:1691-1698(1996).
 CC -!- FUNCTION: Member of the two-component regulatory system rcsc/rcsB
 CC involved in the regulation of the expression of genes involved in
 CC colanic acid capsule synthesis. RscC probably functions as a
 CC membrane-associated protein kinase that phosphorylates rcsB in
 CC response to environmental signals.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Probable).
 CC -!- PTM: Activation probably requires a transfer of a phosphate group
 CC between a His in the transmitter domain and an Asp of the receiver
 CC domain (By similarity).
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC -----
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EMBL	AL627274	CAD07502.1	-
EMBL	AE016836	AAO68299.1	-
EMBL	X87830	CAA61095.1	-
HSSP	P06143	1UDR	
InterPro	IPR003594	ATPbind ATPase	
InterPro	IPR004358	Bact_sens_pr_C	
InterPro	IPR003651	His_kinA	
InterPro	IPR005457	His_kinase	
InterPro	IPR000014	PAS_domain	
InterPro	IPR001789	Response_reg	
Pfam	PF02518	Harpase_c	1
Pfam	PF0512	HiskA	1
Pfam	PF00072	response_reg	1
PRINTS	PR00344	CTRLSENSOR	
ProDom	PD000039	Response_reg	1
SMART	SM00387	HATPase_c	1
SMART	SM00388	HiskA	1
SMART	SM00448	REC_1	
PROSITE	PS0109	HIS_KIN	1
PROSITE	PS0112	PAS	FALSE NEG.
PROSITE	PS0110	RESPONSE REGULATORY	1
KW	Sensory transduction; transferase; Kinase; Bacterial capsule;		
KW	Inner membrane; Transmembrane; Phosphorylation; Complete proteome.		
FT	DOMAIN	1 20	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	21 41	POTENTIAL.
FT	DOMAIN	42 313	PERIPLASMIC (POTENTIAL).
FT	TRANSMEM	314 334	POTENTIAL.
FT	DOMAIN	335 948	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	357 425	PAS.
FT	DOMAIN	476 692	HISTIDINE KINASE.
FT	DOMAIN	826 940	RESPONSE REGULATORY.
FT	MOD RES	479 479	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD RES	875 875	PHOSPHORYLATION (BY SIMILARITY).
FT	SEQUENCE	948 AA	106237 MW; AE3A21701365A865 CRC64;

RESULT 4	RCSC_SALTY	STANDARD;	PRT;	948 AA.
ID	RCSC_SALTY	STANDARD;	PRT;	948 AA.
AC	PS8662;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Sensor protein rcsc (EC 2.7.3.-) (Capsular synthesis regulator component C).			
DE	RCSC OR STM2271.			
GN	Salmonella typhimurium.			
OS	Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Salmonella.			
CC	NCBI_TaxID=602;			
OX	[1]			
RN	SEQUENCE FROM N. A.			
RP	STRAIN=L72 / SGSC1412 / ATCC 700720;			
RC	MEDLINE=12534948; PubMed=11677609;			
RX	McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,			
RA	Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,			

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.: The complete genome sequence of *Salmonella enterica* serovar Typhimurium LT2." *Nature* 413:852-856 (2001).

-!- FUNCTION: Member of the two-component regulatory system rscC/rscB involved in the regulation of the expression of genes involved in colanic acid capsule synthesis. RscC probably functions as a membrane-associated protein kinase that phosphorylates rscB in response to environmental signals.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane. (Probable).

-!- PM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity).

-!- SIMILARITY: Contains 1 histidine kinase domain.

-!- SIMILARITY: Contains 1 PAS (PRR-ARNT-SIM) dimerization domain.

-!- SIMILARITY: Contains 1 response regulatory domain.

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EMBL; AE008801; AL211172.1; .	
StyGene; SG27772; xc8C	
InterPro; IPR003594; Arpbind_ATPase.	
InterPro; IPR004359; Bact_sens_dr_C.	
InterPro; IPR003661; His_kinA.	
InterPro; IPR005467; His_kinase.	
InterPro; IPR000014; PAS_domain.	
InterPro; IPR001789; Response_reg.	
Pfam; PF02518; HATPase_c; 1.	
Pfam; PF00512; HiskA; 1.	
Pfam; PF00072; response_reg; 1.	
PRINTS; PR00344; BCTRLSENSOR.	
ProDom; PD000039; Response_reg; 1.	
SMART; SM00387; HATPase_c; 1.	
SMART; SM00388; HiskA; 1.	
SMART; SM00448; REG; 1.	
PROSITE; PS50109; HIS_KIN; 1.	
PROSITE; PS50112; PAS_FALSE NEG.	
PROSITE; PS50110; RESPONSE_REGULATORY; 1.	
Sensory transduction; Transferrase; Kinase; Bacterial capsule;	
Inner membrane; Transmembrane; Phosphorylation; Complete proteome.	
DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).	
TRANSMEM 21 41 POTENTIAL.	
DOMAIN 42 313 PERIPLASMIC (POTENTIAL).	
TRANSMEM 314 334 POTENTIAL.	
DOMAIN 335 948 CYTOPLASMIC (POTENTIAL).	
DOMAIN 357 425 PAS.	
DOMAIN 476 692 HISTIDINE KINASE.	
DOMAIN 826 940 RESPONSE REGULATORY.	
MOD RES 479 479 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).	
MOD RES 875 875 PHOSPHORYLATION (BY SIMILARITY).	
SEQUENCE 948 AA; 106279 MW; BAAD8DA557D58668 CFC64;	

Qy 78 STTKUREMEYKSMIVCVTSLADNEEBERRAFNEAGLNHCLAKPLTKD 124
|::: :: : |::: |::: |::: |::: |::: |::: |::: |
Db R85 RI.TORTIOLGTLPVGVYTANALAEERKC-DESGMDSCLSKEPWLTD 930

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RESULT 5
RCSC ECOLI STANDARD; PRT; 949 AA.
LC P14376; P76457; P97170; P97202; Q47586;
JT 01-JAN-1990 (Rel. 13, Created)
JT 28-FEB-2003 (Rel. 41, Last sequence update)
JT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator
DE component C).
XN RCSC OR B2218.
XS Escherichia coli.
XC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
XC Enterobacteriaceae; Escherichia.
XX NCBI_TaxID=562;
XN [1]
XP SEQUENCE FROM N.A.
XC STRAIN=K12;
XX MEDLINE=90130299; PubMed=2404948;
XA Stout V., Gottesman S.
XT "RcsB and RcsC: a two-component regulator of capsule synthesis in
XT Escherichia coli.";
XN J. Bacteriol. 172:659-669 (1990).
XN [2]
XP SEQUENCE FROM N.A.
XC STRAIN=O9:K30:H12;
XX MEDLINE=93374832; PubMed=8366025;
XA Jayaratne P., Keenleyside W.J., MacLachlan P.R., Dodgson C.,
XA Whitfield C.;
XT "Characterization of rcsB and rcsC from Escherichia coli O9:K30:H12
XT and examination of the role of the rcs regulatory system in
XT expression of group I capsular polysaccharides.";
XN J. Bacteriol. 175:5384-5394 (1993).
XN [3]
XP SEQUENCE FROM N.A.
XC STRAIN=K12 / MG1655;
XA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
XA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
XA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
XA Mau B., Shao Y.;
XT "The complete genome sequence of Escherichia coli K-12.";
XN Science 277:1453-1474 (1997).
XN [4]
XP SEQUENCE FROM N.A.
XC STRAIN=K12;
XX MEDLINE=97251358; PubMed=9097040;
XA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
XA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
XA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
XA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampaio G., Seki Y.,
XA Sivasubraman S., Tagami H., Takeda J., Takemoto K., Wada C.,
XA Yamamoto Y., Horiuchi T.;
XT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
XT corresponding to the 40.1-50.0 min region on the linkage map.";
XN DNA Res. 3:379-392 (1996).
XC -!- FUNCTION: Member of the two-component regulatory system rcsC/rcsB
CC involved in the regulation of the expression of genes involved in
CC colanic acid capsule synthesis. RcsC probably functions as a
CC membrane-associated protein kinase that phosphorylates rcsB in
CC response to environmental signals.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -!- PTM: Activation probably requires a transfer of a phosphate group
CC between a His in the transmitter domain and an Asp of the receiver
CC domain (By similarity).
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC -!- SIMILARITY: Contains 1 response regulatory domain.
CC -!- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 808.
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CC EMBL; M28242; AAA4503.1; ALT_INIT.
DR EMBL; L11272; AAA4505.1; ALT_INIT.
DR EMBL; AE003111; AAC75278.1; ALT_INIT.
DR EMBL; D90850; BAA16001.1; ALT_FRAME.
DR EMBL; D90850; BAA16006.1; ALT_FRAME.
DR EMBL; D90851; BAA16009.1; ALT_FRAME.
DR EMBL; D90851; BAA16014.1; ALT_FRAME.
DR HSP; P06143; IUDR.
DR EcoGene; EG10822; rcsC.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003661; His_KinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HistPase_c; 1.
DR Pfam; PF00512; HiskA; 1.
DR PRINTS; PR00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HistPase_c; 1.
DR SMART; SM00388; HiskA; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0112; PAS; FALSE NEG.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW Sensory transduction; Transferase; Kinase; Bacterial capsule;
KW Inner membrane; Transmembrane; Phosphorylation; Complete proteome.
FT DOMAIN 1 19 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 20 41 POTENTIAL.
FT DOMAIN 42 313 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 314 335 POTENTIAL.
FT DOMAIN 336 949 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 357 425 PAS.
FT DOMAIN 476 692 HISTIDINE KINASE.
FT DOMAIN 826 940 RESPONSE REGULATION.
FT MOD RES 479 479 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD RES 875 875 PHOSPHORYLATION (BY SIMILARITY).
FT VARIANT 315 315 L -> V (IN STRAIN O9:K30:H12).
FT VARIANT 776 776 K -> E (IN STRAIN O9:K30:H12).
FT VARIANT 890 890 I -> T (IN STRAIN O9:K30:H12).
FT VARIANT 938 938 L -> V (IN STRAIN O9:K30:H12).
FT VARIANT 948 948 D -> E (IN STRAIN O9:K30:H12).
FT CONFLICT 129 130 MR -> IG (IN REF. 1 AND 2).
FT CONFLICT 935 935 T -> S (IN REF. 1).
SQ SEQUENCE 949 AA; 106506 MW; E37E9D70EC944A78 CRC64;
Query Match 25.3%; Score 171.5; DB 1; Length 949;
Best Local Similarity 33.9%; Pred. No. 8.6e-07;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;
QY 18 VLIVDDPPLNLIIEKIKIKAIGIGISQATANGSEAVIHRDGGSSFDLIMDKEMPERDGV 77
Db 827 ILVVDHPINRLLADQLGSLGYQCKTANGVDALNVL--SKNHIDIVLSDVNMFMNDGY 884
QY 78 STTKKLRMEVKSMIVGVTSLNADNEERAEAFEGNHLAKPLTKDKI 126
Db 885 RLQRIKQLGLTLPVIGVTANALAEKQRC-LESGNDSCLSKPVLDDVI 932
RESULT 6
ID FRZE MYXXA STANDARD; PRT; 777 AA.
AC P18769;
DT 01-NOV-1990 (Rel. 16, Created)

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DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gliding motility regulatory protein (EC 2.7.3.-).
 GN PRZE
 OS Myxococcus xanthus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
 OC Cytochrome c; Myxococcaceae; Myxococcus.
 OX NCBI_TaxID=34;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90332690; PubMed=2165608;
 RA McCleary W.R., Zusman D.R.;
 RT "FrzE of Myxococcus xanthus is homologous to both CheA and CheY of
 RT Salmonella typhimurium";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5898-5902(1990).
 RN [2]
 RP PHOSPHORYLATION OF HIS-49.
 RX MEDLINE=91072208; PubMed=2123853;
 RA McCleary W.R., Zusman D.R.;
 RT "Purification and characterization of the Myxococcus xanthus FrzE
 RT protein shows that it has autophosphorylation activity";
 RL J. Bacteriol. 172:6661-6668(1990).
 CC -!- FUNCTION: FRZE IS INVOLVED IN A SENSORY TRANSDUCTION PATHWAY THAT
 CC CONTROLS THE FREQUENCY AT WHICH CELLS REVERSE THEIR GLIDING
 CC DIRECTION. FRZE SEEMS TO BE CAPABLE OF AUTOPHOSPHORYLATING ITSELF
 CC ON AN HISTIDINE RESIDUE AND THEN TO TRANSFER THAT GROUP TO AN
 CC ASPARTATE RESIDUE IN THE C-TERMINAL PART OF THE PROTEIN.
 CC -!- SIMILARITY: Contains 1 cheW-like domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -!- SIMILARITY: Contains 1 HPT domain.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
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 CC
 DR EMBL; M35192; AAA25396.1; -.
 DR PIR; A35966; A35966.
 DR HSSP; Q36310; LB30.
 DR InterPro; IPR003594; ATbind_ATPase.
 DR InterPro; IPR004358; Bact_sens_pr_C.
 DR InterPro; IPR002545; CheW.
 DR InterPro; IPR005467; His_kinase.
 DR InterPro; IPR002570; Hpt.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF01584; CheW; 1.1.ee
 DR Pfam; PF02518; HAIFase_c; 1.
 DR Pfam; PF01627; Hpt; 1.
 DR Pfam; PF00072; response_reg; 1.
 DR PRINTS; PR00344; BCTR1SENSOR.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00260; CheW; 1.
 DR SMART; SM00387; HAIFase_c; 1.
 DR SMART; SM00073; HPT; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS00851; CHEW; 1.
 DR PROSITE; PS0109; HIS_KIN; 1.
 DR PROSITE; PS00894; HPT; 1.
 DR PROSITE; PS01110; RESPONSE_REGULATORY; 1.
 KW Sensory transduction; Transferase; Kinase; Phosphorylation.
 FT DOMAIN 1 108
 FT HPT
 FT DOMAIN 270 509
 FT HISTIDINE KINASE.
 FT DOMAIN 511 645
 FT CHEW-LIKE.
 FT DOMAIN 660 776
 FT RESPONSE REGULATORY.
 FT MOD_RES 49 49
 FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT DOMAIN 130 197
 FT ALA/PRO-RICH (POSSIBLE HINGE REGION).
 SQ SEQUENCE 777 AA; 83189 MW; 9912BD40991C69E5 CRC64;
 Query Match 23.1%; Score 156.5; DB 1; Length 777;
 Best Local Similarity 35.2%; Pred. No. 1.2e-05;
 Matches 38; Conservative 27; Mismatches 38; Indels 5; Gaps 3;
 QY 14 KKLNVLIIVDDPLNLIHETIIKAIGISOTANGGEAVIHRDGGSPDLILMDKEMPE 73
 DB 657 KRLRVLIIVDDSPINATREGALVKGHSVEEQDGEAVV--KVQNTYDILLITDVQMEK 714
 QY 74 RDGVSTTKKUREMEVKSMI--VGVTSIADNEERRAFMEAGLNHCLAK 119
 DB 715 LDGFSLARLRKSTPAVARIPVILISLASPEDKRRG-LDAGADAYLVK 761
 RESULT 7
 ID SKN7_YEAST STANDARD; PRT; 622 AA.
 AC P38889; P39747;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative transcription factor SKN7 (POS9 protein).
 GN SKN7 OR POS9 OR BRV1 OR YHR206W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94042854; PubMed=8226633;
 RA Brown J.L., North S., Bussey H.;
 RT "SKN7, a yeast multicopy suppressor of a mutation affecting cell wall
 RT beta-glucan assembly, encodes a product with domains homologous to
 RT prokaryotic two-component regulators and to heat shock transcription
 RT factors";
 RL J. Bacteriol. 175:6908-6915(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Krens B., Charizanis C., Entian K.-D.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
 RA Kucaba T., Hillier L., Jiler M., Johnston L., Langston Y.,
 RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
 RA Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT VIII";
 RL Science 265:2077-2082(1994).
 RN [4]
 RP FUNCTION, AND MUTAGENESIS.
 RX MEDLINE=95045411; PubMed=7957083;
 RA Brown J.L., Bussey H., Stewart R.C.;
 RT "Yeast Skn7p functions in a eukaryotic two-component regulatory
 RT pathway";
 RL EMBO J. 13:5186-5194(1994).
 CC -!- FUNCTION: INVOLVED IN OXIDATIVE STRESS. TRANSCRIPTION FACTOR THAT
 CC MAY FUNCTION IN A TWO-COMPONENT SIGNAL TRANSDUCTION PATHWAY THAT
 CC ACTS IN PARALLEL WITH THE PKC1 CASCADE TO REGULATE GROWTH AT THE
 CC CELL SURFACE.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC
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 CC

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CC      EMBL; U00485; AAC48911.1; -
DR      EMBL; X83031; CA858143.1; -
DR      EMBL; U00029; AAB69734.1; -
DR      PIR; A49344; A49344.
DR      HSSP; F22121; 2HTS.
DR      SGD; S0001249; SKN7.
DR      GO; GO:0005634; C:nucleus; IDA.
DR      GO; GO:0003709; F:transcription factor activity; IDA.
DR      GO; GO:0000150; F:two-component response regulator activity; IDA.
DR      GO; GO:0006350; P:transcription; IDA.
DR      InterPro; IPR002342; HSF DNA Bind.
DR      InterPro; IPR002341; HSF ETS.
DR      Pfam; PF00447; HSF DNA-bind; 1.
DR      Pfam; PF00072; response reg; 1.
DR      PRINTS; PR00056; HSFDOMAIN.
DR      ProDom; PD001788; HSF DNA Bind; 1.
DR      SMART; SM00415; HSF; 1.
DR      SMART; SM00448; REC; 1.
DR      PROSITE; PS00434; HSF DOMAIN; 1.
DR      PROSITE; PS0110; RESPONSE REGULATORY; 1.
KW      Transcription regulation; Sensory transduction; Nuclear protein;
KW      DNA-binding; Phosphorylation.
FT      DNA BIND 86 190
FT      DOMAIN 378 492
FT      MOD RES 427 427
FT      MUTAGEN 427 427
FT      MUTAGEN 427 427
SQ      SEQUENCE 622 AA; 69202 MW; 4C732FD6E326742 CRC64;
Query Match 22.1%; Score 150; DB 1; Length 622;
Best Local Similarity 28.1%; Pred. No. 3.3e-05;
Matches 38; Conservative 32; Mismatches 45; Indels 20; Gaps 4;
QY      12 IKKLVLLVDDPLNLIIHKIKAGISQIQTANNGEAVII---HRDGGSSFDLILMD 68
Db      373 LRKGFHVLVEDDAVSIQCKFLKYGCTVQVSDGLSALSTLEKRV-----YDLVMD 427
QY      69 KEMPERDGVSTTKLREMEVKSMIVGVTSFLADNFEERRAFMEAGLNHCLAKPTKYKI-- 126
Db      428 IVPNLDGATATSIVRSDNETPTIAMTGNM--QDLITVQLHGMDILAKPTTRDDLHS 486
QY      127 -----IPLNQ 132
Db      487 ILIRYLKDRIPLCEQ 501
RESULT 8
ARCB_ECO57
ID      ARCB_ECO57 STANDARD; PRT; 778 AA.
AC      F58363;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Aerobic respiration control sensor protein arcb (BC 2.7.3.-).
GN      ARCB OR Z4574 OR BCS4089.
OS      Escherichia coli O157:H7.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=83334;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX      MEDLINE=21074935; PubMed=11206551;
RA      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA      Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA      Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA      Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA      Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA      Welch R.A., Blattner F.R.;

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RT      "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL      Nature 409:529-533 (2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=O157:H7 / RIMD 050952;
RX      MEDLINE=21156231; PubMed=11258796;
RA      Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA      Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA      Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA      Kuhara S., Shiba T., Hattori M., Sainagawa H.;
RT      "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT      O157:H7 and genomic comparison with a laboratory strain K-12."
RL      DNA Res. 8:11-22(2001).
CC      -!- FUNCTION: Member of the two-component regulatory system arcb/arcbA.
CC      Sensor-regulator protein for anaerobic repression of the arc
CC      modulon. Activates arcbA via a four-step phosphorylation. ArcB can
CC      also dephosphorylate arcbA by a reverse phosphorylation involving His-
CC      717 and Asp-576 (By similarity).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC      (Probable).
CC      -!- PTM: Activation requires a sequential transfer of a phosphate
CC      group from a His in the primary transmitter domain, to an Asp in
CC      the receiver domain and to a His in the secondary transmitter
CC      domain (By similarity).
CC      -!- SIMILARITY: Contains 1 histidine kinase domain.
CC      -!- SIMILARITY: Contains 1 HTP domain.
CC      -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC      -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC      -!- SIMILARITY: Contains 1 response regulatory domain.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch)
CC      -----
CC      EMBL; AE005549; AAC58344.1; -
CC      EMBL; AP002564; BAB37512.1; -
DR      PIR; A91140; A91140.
DR      PIR; D85985; D85985.
DR      InterPro; IPR003594; ATPbind AtPase.
DR      InterPro; IPR003661; His_kinA.
DR      InterPro; IPR005467; His_kinase.
DR      InterPro; IPR002570; Hpt_kinase.
DR      InterPro; IPR000700; PAS-associ C.
DR      InterPro; IPR000014; PAS_domain.
DR      InterPro; IPR001789; Response_reg.
DR      Pfam; PF02518; HATPase_C; 1.
DR      Pfam; PF00512; HiskA; 1.
DR      Pfam; PF00989; PAS; 1.
DR      Pfam; PF00072; response reg; 1.
DR      ProDom; PD000039; Response_reg; 1.
DR      SMART; SM00387; HATPase_C; 1.
DR      SMART; SM00388; HiskA; 1.
DR      SMART; SM00073; HPT; 1.
DR      SMART; SM00091; PAS; 1.
DR      SMART; SM00448; REC; 1.
DR      TIGRFAMs; TIGR00229; sensory_box; 1.
DR      PROSITE; PS0109; HIS_KIN; 1.
DR      PROSITE; PS0894; HPT; 1.
DR      PROSITE; PS0113; PAC; 1.
DR      PROSITE; PS0112; PAS; 1.
DR      PROSITE; PS0110; RESPONSE REGULATORY; 1.
KW      Sensory transduction; Transference; Kinase; Phosphorylation;
KW      Transmembrane; Inner membrane; Transcription regulation;
KW      Complete proteome.
FT      DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 26 46 POTENTIAL.
FT      DOMAIN 47 57 PERIPLASMIC (POTENTIAL).
FT      TRANSMEM 58 78 POTENTIAL.
FT      DOMAIN 79 778 CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 153 223 PAS.
FT DOMAIN 226 278 PAC.
FT DOMAIN 289 507 HISTIDINE KINASE.
FT DOMAIN 527 643 RESPONSE REGULATORY.
FT DOMAIN 678 771 HPT.
FT MOD_RES 292 292 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 576 576 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 717 717 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 778 AA; 88010 MW; C8AE004B007F9D30 CRC64;

Query Match 22.1%; Score 149.5; DB 1; Length 778;
Best Local Similarity 25.6%; Pred. No. 4.6e-05;
Matches 31; Conservative 40; Mismatches 47; Indels 2;

QY 16 LNVLIYDDPLNLIIEKIIKAIIGISQTANNGEBAVVIHRDGGSSFDLIIMDKEMPERD 75
DB 526 LNVLIYDDPLNLIIEKIIKAIIGISQTANNGEBAVVIHRDGGSSFDLIIMDKEMPERD 583
QY 76 GVSTTKKLEMEVKSMIVGTSIADNE--EERRAFMEAGLNHCLAKPLTKDKIIPLINOLM 134
DB 584 GLDISRELTKRYPRDPLPLVALTANVLKDKQEYLNAGMDDVLKPLSVPALTMIKFW 643
QY 135 D 135
DB 644 D 644

RESULT 9
ARCH_ECOLI STANDARD; PRT; 778 AA.
AC P22763;
DT 01-AUG-1991 (Rel. 19, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aerobic respiration control sensor protein arcbB (EC 2.7.3.-).
GN ARCB OR B3210 OR SP3250.
OS Escherichia coli, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=9035583; PubMed=2201868;
RA Iuchi S., Matsuda Z., Fujiwara T., Lin E.C.C.;
RT "The arcb gene of Escherichia coli encodes a sensor-regulator protein
RL for anaerobic repression of the arc modulon.";
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RX Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA May B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384530;
RA Jin Q., Yuan J., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang X., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [4]
RP CHARACTERIZATION.

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RC SPECIES=E.coli; STRAIN=M15;
RX MEDLINE=97431492; PubMed=9286997;
RA Georgellis D., Lynch A.S., Lin E.C.C.;
RT "In vitro phosphorylation study of the arc two-component signal
RL transduction system of Escherichia coli.";
RN [5]
RP Bacteriol. 179:5429-5435(1997).
RN CHARACTERIZATION.
RC SPECIES=E.coli; STRAIN=M15;
RX MEDLINE=99047671; PubMed=9830034;
RA Georgellis D., Kwon O., De Wulf P., Lin E.C.C.;
RT "Signal decay through a reverse phosphorelay in the arc two-component
RL signal transduction system.";
RN J. Biol. Chem. 273:32864-32869(1998).
RN [6]
RN MUTAGENESIS OF HIS-292; ASP-576 AND HIS-717.
RC SPECIES=E.coli; STRAIN=K12 / MC4100;
RX MEDLINE=20309722; PubMed=10851007;
RA Kwon O., Georgellis D., Lin E.C.C.;
RT "Phosphorelay as the sole physiological route of signal transmission
RL by the arc two-component system of Escherichia coli.";
RN J. Bacteriol. 182:3858-3862(2000).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS) OF 660-778.
RC SPECIES=E.coli;
RX MEDLINE=97207018; PubMed=9054511;
RA Kato M., Mizuno T., Shimizu T., Hakoshima T.;
RT "Insights into multistep phosphorelay from the crystal structure of
RL the C-terminal HPT domain of ArcB.";
RN Cell 88:717-723(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 659-776 IN COMPLEX WITH CHEY.
RC SPECIES=E.coli;
RX MEDLINE=98437504; PubMed=9761838;
RA Kato M., Mizuno T., Hakoshima T.;
RT "Crystallization of a complex between a novel C-terminal transmitter,
RL HPT domain, of the anaerobic sensor kinase ArcB and the chemotaxis
RT response regulator CheY.";
RN Acta Crystallogr. D 54:140-142(1998).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.57 ANGSTROMS) OF 659-776.
RC SPECIES=E.coli;
RX MEDLINE=2003135; PubMed=10531481;
RA Kato M., Mizuno T., Shimizu T., Hakoshima T.;
RT "Refined structure of the histidine-containing-phosphotransfer (HPT)
RL domain of the anaerobic sensor kinase ArcB from Escherichia coli at
RT 1.57-A resolution.";
RN Acta Crystallogr. D 55:1842-1849(1999).
RN [10]
RP FUNCTION: Member of the two-component regulatory system arcbB/arcbA.
RC Sensor-regulator protein for anaerobic repression of the arc
RX modulon. Activates arcbA via a four-step phosphorelay. ArcB can
RL also dephosphorylate arcbA by a reverse phosphorelay involving His-
RX 717 and Asp-576.
RN [11]
RP SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
RX (Probable).
RN [12]
RP PTM: Activation requires a sequential transfer of a phosphate
RX group from a His in the primary transmitter domain, to an Asp in
RL the receiver domain and to a His in the secondary transmitter
RN domain.
RN [13]
RP SIMILARITY: Contains 1 histidine kinase domain.
RX [14]
RP SIMILARITY: Contains 1 HPT domain.
RX [15]
RP SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
RX [16]
RP SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
RX [17]
RP SIMILARITY: Contains 1 response regulatory domain.
RX [18]
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RN [19]

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DR EMBL; X53315; CAA37397.1; --
DR EMBL; U18997; AAS8012.1; --
DR EMBL; AE000400; AAC76242.1; --
DR EMBL; AE015336; AAN44715.1; --
DR FIR; D65112; RGCAR.
DR PDB; IACB; 18-MAR-98.
DR PDB; 2ACB; 17-JUN-98.
DR PDB; 1BDJ; 11-MAY-99.
DR PDB; 1FRO; 31-DEC-02.
DR EcoGene; EG10062; atcB.
DR InterPro; IPR003594; AtPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003661; His_KinA.
DR InterPro; IPR005467; His_Kinase.
DR InterPro; IPR002570; Hpt.
DR InterPro; IPR000700; PAS-associ C.
DR InterPro; IPR000014; PAS domain.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HiskA; 1.
DR Pfam; PF00989; PAS; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR PRINTS; PR000039; Response_reg; 1.
DR SMART; SM00388; HiskA; 1.
DR SMART; SM00093; HPT; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00448; REC; 1.
DR TIGRfams; TIGR00229; sensory_box; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50894; HPT; 1.
DR PROSITE; PS50113; PAC; 1.
DR PROSITE; PS50112; PAS; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
DR Sensory transduction; Transferrase; Kinase; Phosphorylation;
KW Transmembrane; Inner membrane; Transcription regulation; 3D-structure;
KW Complete proteome.
FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 26 46 POTENTIAL.
FT DOMAIN 47 57 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 58 78 POTENTIAL.
FT DOMAIN 79 778 POTENTIAL.
FT DOMAIN 153 223 PAS.
FT DOMAIN 226 278 PAC.
FT DOMAIN 289 507 HISTIDINE KINASE.
FT DOMAIN 527 643 RESPONSE REGULATORY.
FT DOMAIN 678 771 HPT.
FT MOD_RES 292 292 PHOSPHORYLATION (AUTO-).
FT MOD_RES 576 576 PHOSPHORYLATION (PROBABLE).
FT MOD_RES 717 717 PHOSPHORYLATION (PROBABLE).
FT MUTAGEN 292 292 H->Q: LOSS OF ACTIVITY.
FT MUTAGEN 576 576 D->A: LOSS OF ACTIVITY.
FT MUTAGEN 717 717 H->Q: LOSS OF ACTIVITY.
FT CONFLICT 469 470 MISSING (IN REF. 2).
SQ SEQUENCE 778 AA; 873982 MW; D661EAG6CF9AD30 CRC64;

Query Match 22.1%; Score 149.5; DB 1; Length 778;
Best Local Similarity 25.6%; Pred. No. 4.6e-05;
Matches 31; Conservative 40; Mismatches 47; Indels 3; Gaps 2;

QY 16 LNVLLVDDPDLNLIHEKIIKAIIGGIGQTANNGEAVIIHRDGGSSFDLLMDKEMPERD 75
Db * 526 LNVLLVDDPDLNLIIVARSVLKSGNSVDVMTGKAALMEKPKG--EYDLVLLDIQLPDMT 583
QY 76 GYSTTKKLREMEKSMIVGVTSLADNE--EERRAFMEAGLNHCLAKPLTKDKIPLINQLM 134
Db 584 GLDISRELTKRYPREDLPLPALVTANVLKDKQEVNAGMDVLLSKPLSVLPALTAMIKKEW 643
QY 135 D 135
Db 644 D 644

RESULT 10
SLN1_YEAST STANDARD; PRT; 1220 AA.
AC P39928;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Osmolarity two-component system protein SLN1 (EC 2.7.3.-).
GN SLN1 OR YPD2 OR YII147C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
[1]
SEQUENCE FROM N.A.
RC STRAIN=S288C / YPH1;
RX MEDLINE=94024010; PubMed=8211183;
RA Ota I.M., Varshavsky A.;
RT "A yeast protein similar to bacterial two-component regulators.";
RL Science 262:566-569(1993).
[2]
SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX PubMed=9169870;
RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
RL Nature 387:84-87(1997).
[3]
MUTAGENESIS OF HIS-576 AND ASP-1144.
RX MEDLINE=94239498; PubMed=8183345;
RA Maeda T., Wurgler-Murphy S.M., Saito H.;
RT "A two-component system that regulates an osmosensing MAP kinase
RT cascade in yeast.";
RL Nature 369:242-245(1994).
CC -!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
CC SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE
CC EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SSK2/SSK22->
CC PBS2->HOG1 PATHWAY. INACTIVE SLN1 ALLOWS THE UNPHOSPHORYLATED SSK1
CC PROTEIN TO ACTIVATE SSK2 AND SSK22, TWO MAPKKS THAT FURTHER
CC STIMULATE THE PBS2->HOG1 MAPK CASCADE. IN LOW OSMOLARITY MEDIA,
CC THE ACTIVATED SLN1 HISTIDINE KINASE REPRESSSES THE ACTIVATION OF THE
CC PBS2->HOG1 KINASE CASCADE THROUGH PHOSPHORYLATION OF SSK1.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP
CC BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND AN ASP OF THE RECEIVER
CC DOMAIN.
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
CC -!- SIMILARITY: Contains 1 response regulatory domain.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; Z38059; CAA86131.1; --
CC EMBL; U01835; AAC48912.1; --
CC FIR; S48387; S48387.
CC HSSP; P06143; 1UDR.
CC SGD; S0001409; SLN1.
CC GO; GO:0007234; P:osmosensory signaling pathway via two-compo. . .; IDA.
CC GO; GO:0042542; P:response to hydrogen peroxide, IMP.
CC InterPro; IPR003594; AtPbind_ATPase.
CC InterPro; IPR004358; Bact_sens_pr_C.
CC InterPro; IPR003661; His_KinA.
CC InterPro; IPR005467; His_Kinase.
CC InterPro; IPR001789; Response_reg.
```


28-FEB-2003 (Rel. 41, Last annotation update)
Sensor protein gacs (EC 2.7.3.-).
GACS OR LEVA.
Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
[1]
SEQUENCE FROM N.A.
MEDLINE=92234961; PubMed=1314807;
Hrabak E.M., Willis D.K.;
"The leaA gene required for pathogenicity of Pseudomonas syringae pv.
syringae on bean is a member of a family of two-component
regulators.";
J. Bacteriol. 174:3011-3020(1992).
CC -!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
GACS/GACS (LEVA). MAY BE INVOLVED IN LESION FORMATION, SWARMING AND
IN THE PRODUCTION OF EXTRACELLULAR PROTEASE, SYRINGOMYCIN AND N-
ACYL-L-HOMOSERINE LACTONE (ACYL-HSL). REQUIRED FOR PATHOGENICITY
ON BEAN.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
(Probable).
CC -!- PTM: Activation requires a sequential transfer of a phosphate
group from a His in the primary transmitter domain, to an Asp in
the receiver domain and to a His in the secondary transmitter
domain (By similarity).
CC -!- SIMILARITY: Contains 1 HAMP domain.
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
CC -!- SIMILARITY: Contains 1 HPT domain.
CC -!- SIMILARITY: Contains 1 response regulatory domain.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M80477; AAA25877.1; -;
DR HSSP; P06143; LUDR;
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003660; HAMP.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005457; His_kinase.
DR InterPro; IPR002570; Hpt_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00387; Harpase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR SMART; SM00073; HPT; 1.
DR PROSITE; PS00885; HAMP; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50894; HPT; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Sensory transduction; Transferase; Kinase; Phosphorylation;
Transmembrane; Inner membrane.
FT TRANSMEM 9 25 POTENTIAL.
FT TRANSMEM 84 101 POTENTIAL.
FT TRANSMEM 159 178 POTENTIAL.
FT DOMAIN 182 234 HAMP.
FT DOMAIN 281 502 HISTIDINE KINASE.
FT DOMAIN 658 777 RESPONSE REGULATORY.
FT DOMAIN 814 907 HPT.

FT MOD_RES 284 284 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
DE MOD_RES 707 707 PHOSPHORYLATION (BY SIMILARITY).
GN MOD_RES 853 853 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 907 AA; 99195 MW; 559F4663DAF3492C CRC64;
Query Match 20.9%; Score 142; DB 1; Length 907;
Best Local Similarity 27.6%; Pred. No. 0.00023;
Matches 35; Conservative 33; Mismatches 33; Indels 26; Gaps 4;
QY 18 VLIIVDDPPLNLIHEIKIIGISQTNNGEEAVIHRDGG-----SSFDILMD 68
DB 659 VLVCDPDPANLLVQTLLEDVG-----AEVVAVGGYAANVAQOEAFDVLMD 707
QY 69 KEMPERGVSTTKKLEMEVKS-----MIVGVTSLDNNEERAFMEAGNHLCLAPLTK 123
DB 708 VQFMGMDGRQATEAIRAEAEARNQSSLPFIVALTAAH-MANEKRSILQSGMDDYLTKEISE 766
QY 124 DKTIPLI 130
DB 767 RQLAQVV 773
RESULT 13
DCTR BACSU STANDARD; PRT; 226 AA.
AC P96502; P94503;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable C4-dicarboxylate response regulator dctr.
DCTR.
GN Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]_TaxID=1423;
RP SEQUENCE FROM N.A.
RT STRAIN=168;
RA Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
RT "A 148 kbp sequence of the region between 35 and 47 degree of the
Bacillus subtilis genome".
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=980404033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Knaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maubert J., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Furrelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler H., Wedler H., Weitzengger I.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

```

RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RL subtilis";
RN Nature 390:249-256 (1997).
RP [3].
RN SEQUENCE OF 14-101 FROM N.A.
RC STRAIN=SB202;
RX MEDLINE=97311990; PubMed=9168601;
RA Morel-Deville F., Ehrlich S.D., Morel P.;
RT "Identification by PCR of genes encoding multiple response
RL regulators";
RN Microbiology 143:1513-1520 (1997).
RP [4].
RN FUNCTION, AND GENE NAME.
RC STRAIN=168;
RX MEDLINE=20170658; PubMed=10708364;
RA Asai K., Baik S.-H., Kasahara Y., Moriya S., Ogasawara N.;
RT "Regulation of the transport system for C4-dicarboxylic acids in
RL Bacillus subtilis";
RN Microbiology 146:263-271 (2000).
CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
CC ESSENTIAL FOR EXPRESSION OF DCTP.
CC -1- PTM: PHOSPHORYLATED BY DCTS (PROBABLE).
CC -1- SIMILARITY: Contains 1 response regulatory domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB001488; BAA12983.1; -.
DR EMBL; Z99106; CAB12253.1; -.
DR EMBL; U82580; AAB41751.1; -.
DR PIR; B69771; B69771.
DR HSP; Q56312; ITMY.
DR Subtilisin; BG12074; dctR.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; response_reg.1
DR PIRSF; PIRSF006171; RR_Citrat_malat; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0110; RESPONSE REGULATORY; 1.
DR SENSORY transduction; Transcription regulation; DNA-binding;
KW Activator; Phosphorylation; Complete proteome.
FT DOMAIN 7 123 RESPONSE REGULATORY
FT MOD RES 58 58 PHOSPHORYLATION (BY SIMILARITY).
FT DNA_BIND 176 206 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 24 24 F -> I (IN REF. 3).
SQ SEQUENCE 226 AA; 25539 MW; 018115B14B9EF47D CRC64;

Query Match 20.7%; Score 140.5; DB 1; Length 226;
Best Local Similarity 25.9%; Pred. No. 6.7e-05;
Matches 30; Conservative 39; Mismatches 42; Indels 5; Gaps 3;

QY 13 KKKLVIVDDDDPLNLIHKKIKAIGGTS--CTANNGEAVIHRDGGSSFDLILMDKE 70
DB 3 RKKVLLIEDDPVQVYVNRKDFITTVKGVTVCATAGNGBEGLKIKE--EQPDVLVDVY 60

QY 71 MPRDGVSTTKKLRMEVKSMTVGVTSKADNEERRAFMEAGLNHCLAKPLTKDKI 126
DB 61 MPKDGKIKTLQIRKQKLEVDVI-VVSAKDKETISLMLQNGAVYILKPFKLEEM 115

RESULT 14
DCTR_BACHD STANDARD; PRT; 230 AA.
AC Q9K938;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Probable C4-dicarboxylate response regulator dctr.
GN DCTR OR BH2751.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1].
RN SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RL halodurans and genomic sequence comparison with Bacillus subtilis.";
RN Nucleic Acids Res. 28:4317-4331 (2000).
CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
CC ESSENTIAL FOR EXPRESSION OF DCTP (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- PTM: PHOSPHORYLATED BY DCTS (By similarity).
CC -1- SIMILARITY: Contains 1 response regulatory domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; AP001516; BAB06470.1; -.
DR PIR; G83993; G83993.
DR HSP; P10957; 1RNL.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; response_reg.1
DR PIRSF; PIRSF006171; RR_Citrat_malat; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0110; RESPONSE REGULATORY; 1.
DR SENSORY transduction; Transcription regulation; DNA-binding;
KW Activator; Phosphorylation; Complete proteome.
FT DOMAIN 8 124 RESPONSE REGULATORY
FT MOD RES 59 59 PHOSPHORYLATION (BY SIMILARITY).
FT DNA_BIND 183 209 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 230 AA; 26376 MW; 06FD65F46FC57D40 CRC64;

Query Match 20.7%; Score 140.5; DB 1; Length 230;
Best Local Similarity 29.4%; Pred. No. 6.9e-05;
Matches 35; Conservative 32; Mismatches 47; Indels 5; Gaps 3;

QY 16 LNVILVDDDDPLNLIHKKIKAIGG--ISQTANNGEAVIHRDGGSSFDLILMDKEMPE 73
DB 7 IRVLLIEDDPVQVYVNRMFVKLSGFTTIVGTATGEGMVKTRE--LQPDLLILDIFMPK 64

QY 74 RGVSTTKKLRMEVKSMTVGVTSKADNEERRAFMEAGLNHCLAKPLTKDKIPLNQ 132
DB 65 QDGLSFQIRQYIVDVIIVTA-ANDTKIKLLRYGVWDYLVKPFTEPLKAAITQ 122

RESULT 15
CHEY_BACSU STANDARD; PRT; 119 AA.
ID CHEY_BACSU
DT P24072; P37583;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotaxis protein cheY homolog.
GN CHEY OR CHEB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1].
RN SEQUENCE FROM N.A.
RC STRAIN=168 / O11085;

```

XX MEDLINE=91286247; PubMed=1905718;

RA Bischoff D.S., Ordal G.W.;

RT "Sequence and characterization of *Bacillus subtilis* CheB, a homolog of *Escherichia coli* CheY, and its role in a different mechanism of chemotaxis.";

RL J. Biol. Chem. 266:12301-12305(1991).

RL (2)

RP SEQUENCE FROM N.A.

RC STRAIN=168;

XX MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Moszer J., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Broussier L., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brummett S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.X., Codani J.J., Conerton I.P., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,

RA Enriani K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallazzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Giuseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kaashara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningsstein G., Krohn S., Kumano M.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,

RA Noone D., O'Reilly M., Ogawa K., Ogawa A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetle D., Porwollik S., Prescott A.M.,

RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,

RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Takakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzneger T.,

RA Winters P., Wipat K., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,

RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.";

RL Nature 390:249-256(1997).

RL (3)

RP SEQUENCE OF 1-7 FROM N.A.

RC STRAIN=168 / OI1085;

RX MEDLINE=93078625; PubMed=1447979;

RA Bischoff D.S., Ordal G.W.;

RT "Identification and characterization of *FlhY*, a novel component of the *Bacillus subtilis* flagellar switch complex.";

RL Mol. Microbiol. 6:2715-2723(1992).

RL (4)

RP SEQUENCE OF 95-119 FROM N.A.

RC STRAIN=168 / OI1085;

RX MEDLINE=92283757; PubMed=1597417;

RA Bischoff D.S., Weinreich M.D., Ordal G.W.;

RT "Nucleotide sequences of *Bacillus subtilis* flagellar biosynthetic genes *flp* and *fliQ* and identification of a novel flagellar gene, *flhZ*.";

RL J. Bacteriol. 174:4017-4025(1992).

RL (5)

RP SEQUENCE OF 1-12.

RC STRAIN=168 / JH642;

RX MEDLINE=96345629; PubMed=8755892;

RA Gramann P., Schroeder K., Schmid R., Marahel M.A.;

RT "Cold shock stress-induced proteins in *Bacillus subtilis*.";

RL J. Bacteriol. 178:4611-4619(1996).

CC -!- FUNCTION: HAS A CENTRAL CONTROLLING ROLE IN CHEMOTAXIS. ALTHOUGH

CC IT IS HOMOLOGOUS TO THE CHEY PROTEIN OF OTHER BACTERIA, IT IS

CC THOUGHT TO FUNCTION IN A DIFFERENT MANNER.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Contains 1 response regulatory domain.

CC -----

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CC -----

DR EMBL; M59781; AAA22311.1; -

DR EMBL; Z99112; CAB13506.1; -

DR EMBL; M8738; AAA22450.1; -

DR EMBL; M87005; AAA22451.1; -

DR PIR; A40874; A40874.

DR HSSP; Q56312; ITMY.

DR Subtilist; BG10258; cheY.

DR InterPro; IPR001789; Response reg.

DR Pfam; PF00072; response reg. 1.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS0110; RESPONSE REGULATORY; 1.

KW Chemotaxis; Sensory transduction; Phosphorylation; Complete proteome.

FT INIT MET 0 118 RESPONSE REGULATORY.

FT MOD RES 53 53 PHOSPHORYLATION (BY SIMILARITY).

EQ SEQUENCE 119 AA; 13178 MW; F3BCA0F02CAB7531 CRC64;

Query Match 19.8%; Score 134; DB 1; Length 119;

Best Local Similarity 26.9%; Pred. No. 0.00012;

Matches 32; Conservative 36; Mismatches 47; Indels 4; Gaps 3;

QY 18 VLIVDDDP-LNLIHKKIKAGIGISQTANNCEAAVIIHRDGGSSFDLILMDKEMPERDG 76

Db 4 ILIVDDDAFWRMKILVKNGEVVAEENGAQAVEKYKE--HSPDLVTMDITWPEMDG 61

QY 77 VSTTKKLREMEVSMIVGVTSVLADNEEERAEAGLNECLAKPLTKKILPLINQLMD 135

Db 62 ITALKEIKQIDAQARIIMCSAMGQSQMWIDA-IQAGAKDFIVKPFQADRVLEINKTLN 119

Search completed: August 14, 2003, 16:47:19

Job time : 24 secs

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	181	26.7	1969	1	T08875	histidine kinase h
2	178.5	26.3	1197	2	G65010	sensor protein evg
3	176.5	26.0	1197	2	A91035	probable sensor fo
4	176.5	26.0	1197	2	C85879	probable sensor fo
5	174	25.7	394	2	H87640	sensor histidine k
6	173.5	25.6	948	2	AD0790	sensor protein rcs
7	171.5	25.3	933	1	BVECCC	sensor protein rcs
8	171.5	25.3	933	2	C91017	sensor for ctr cap
9	171.5	25.3	933	2	E85961	hypothetical prote
10	171.5	25.3	957	2	AD0149	two component sens
11	162.5	24.0	642	2	E87644	sensor box histid
12	162.5	24.0	778	2	AD0432	aerobic respiratio
13	159	23.5	117	2	A69487	response regulator
14	159	23.5	736	2	C83151	sensor histidine k
15	159	23.5	1645	2	AG8397	two-component hybr
16	157	23.2	900	2	B87252	sensor box histid
17	156.5	23.1	777	2	A35966	chemotaxis protein
18	155	22.9	690	2	A87580	sensor box histid
19	154.5	22.8	122	2	G69422	response regulator
20	154.5	22.8	572	2	E82198	sensor histidine k
21	153.5	22.6	713	2	A87617	sensor box histid
22	152.5	22.5	110	1	S58645	response regulator
23	152.5	22.5	120	2	G84253	chemotaxis protein
24	152.5	22.5	534	2	A87266	sensor histidine k
25	152	22.4	1014	1	S75023	sensor transducti
26	151.5	22.3	633	2	S75525	sensor transducti
27	150.5	22.2	778	2	AG0306	aerobic respiratio
28	150.5	22.2	939	2	AB0032	two-component sens
29	150	22.1	632	1	A49344	cellwall assembly


```

Best Local Similarity 31.7%; Pred. No. 3.4e-07;
Matches 39; Conservative 31; Mismatches 49; Indels 4; Gaps 2;

QY 14 KKLNVLDVDDPLNLIHKEIKATGIGISQATNNGEAAVTHRRDGGSSFDLILMDKEMPE 73
DB 262 RGAHILVDDNATNWEAALCMFECSQEAQVGEAVEWARG--RFDLILMDIKMPR 319
QY 74 RGVSTTKLREMEVKSMTVGVTSIADNEE--ERRAFWEAGLNHCLAKPLTKDKIPLIN 131
DB 320 MDGVAATRAIRELSGRSSAAPFVALTANADPADVHTVLAQMGQDVKEPKIKPERLALVN 379
QY 132 QLM 134
DB 380 SL 382

RESULT 6
AD0790
A:Title: sensor protein RscC (EC 2.7.3.-) [imported] - Salmonella enterica subsp. enterica serovar
A:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AD0790
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0790
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-948 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07502.1; PID:gl6503497; GSPDB:GN00176
C:Genetics:
A:Gene: rscC
A:Superfamily: rscC protein; response regulator homology
C:Keywords: phosphotransferase

Query Match 25.6%; Score 173.5; DB 2; Length 948;
Best Local Similarity 33.9%; Pred. No. 1e-06;
Matches 37; Conservative 33; Mismatches 36; Indels 3; Gaps 2;

QY 18 VLIIVDDPLNLIHKEIKATGIGISQATNNGEAAVTHRRDGGSSFDLILMDKEMPERDGV 77
DB 827 ILVVDHPINRLLADQLGSLGYQCKTANGVDALNVL--SKNAIDIVLSDVNNPNMDGY 884
QY 78 STTKKLREMEVKSMTVGVTSIADNEEERRAFWEAGLNHCLAKPLTKDKI 126
DB 885 RLTORIRQLGTLFVVGVTANALAEKQRC-LESGMDSCLSKPVTLDAL 932

RESULT 7
BVECCC
A:Title: sensor protein rscC (EC 2.7.3.-) - Escherichia coli (strain K-12)
N:Alternate names: regulatory protein rscC
C:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002
C:Accession: H64991; JUV0069; A48659
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A6720; MUID:197426617; PMID:9278503
A:Accession: H64991
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-933 <BLAT>
A:Cross-references: GB:AE000311; GB:U00096; NID:g1788547; PIDN:AAC75278.1; PID:g1788548;
A:Experimental source: strain K-12, substrain MG1655
R:Scout, V.; Gottesman, S.
J. Bacteriol. 172, 659-669, 1990

A:Title: RcsB and RcsC: a two-component regulator of capsule synthesis in Escherichia cc
A:Reference number: JUV068; MUID:90130299; PMID:2404948
A:Accession: JUV069
A:Molecule type: DNA
A:Residues: 1-112, 'IG', 115-918, 'S', 920-933 <STO>
A:Cross-references: GB:M28242; NID:g147524; PIDN:AAA24503.1; PID:g147525
A:Experimental source: strain K12
R:Yavarane, P.; Keenleyside, W.J.; MacLachlan, P.R.; Dodgson, C.; Whitfield, C.
J. Bacteriol. 175, 5384-5394, 1993
A:Title: Characterization of rcsB and rcsC from Escherichia coli O9: K30:H12 and examine
A:Reference number: A48659; MUID:93374832; PMID:8366025
A:Accession: A48659
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-112, 'IG', 115-298, 'V', 300-759, 'E', 761-873, 'T', 875-921, 'V', 923-931, 'E', 933 <
A:Cross-references: GB:L11272; NID:g147527; PIDN:AAA24503.1; PID:g147528
A:Experimental source: strain K30 (O9:K30:H12)
C:Comment: This protein acts as the sensor of the two-component regulatory system to sti
C:Genetics:
A:Gene: rcsC
A:Map position: 48 min
A:Superfamily: rscC protein; response regulator homology
C:Keywords: autophosphorylation; capsule synthesis; phosphohistidine; phosphoprotein; ph
F:4-26/Domain: transmembrane #status predicted <TM2>
F:298-318/Domain: transmembrane #status predicted <TM2>
F:811-920/Domain: response regulator homology <RRH>
F:863/Binding site: phosphate (His) (covalent) #status predicted
F:859/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 25.3%; Score 171.5; DB 1; Length 933;
Best Local Similarity 33.9%; Pred. No. 1.5e-06;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 18 VLIIVDDPLNLIHKEIKATGIGISQATNNGEAAVTHRRDGGSSFDLILMDKEMPERDGV 77
DB 811 ILVVDHPINRLLADQLGSLGYQCKTANGVDALNVL--SKNHIDIVLSDVNNPNMDGY 868
QY 78 STTKKLREMEVKSMTVGVTSIADNEEERRAFWEAGLNHCLAKPLTKDKI 126
DB 869 RLTORIRQLGTLFVVGVTANALAEKQRC-LESGMDSCLSKPVTLDVI 916

RESULT 8
C91017
A:Title: sensor for ctr capsule biosynthesis [imported] - Escherichia coli (strain O157:H7, subst
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: C91017
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-933 <HAY>
A:Cross-references: PIDN:BA000007; PIDN:BA036530.1; PID:g13362576; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:
A:Gene: EC93107
A:Superfamily: rscC protein; response regulator homology

Query Match 25.3%; Score 171.5; DB 2; Length 933;
Best Local Similarity 33.9%; Pred. No. 1.5e-06;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 18 VLIIVDDPLNLIHKEIKATGIGISQATNNGEAAVTHRRDGGSSFDLILMDKEMPERDGV 77
DB 811 ILVVDHPINRLLADQLGSLGYQCKTANGVDALNVL--SKNHIDIVLSDVNNPNMDGY 868
QY 78 STTKKLREMEVKSMTVGVTSIADNEEERRAFWEAGLNHCLAKPLTKDKI 126
DB 869 RLTORIRQLGTLFVVGVTANALAEKQRC-LESGMDSCLSKPVTLDVI 916

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RESULT 13
A69487

Search completed: August 14, 2003, 16:51:17
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 16:49:07 ; Search time 55 Seconds
(without alignments)

323.935 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678

Sequence: 1 MATKSMGDIKKKLVLI.....LAKPLTKDKIPLINQLMDA 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	202	29.8	261	15	US-10-101-464A-127
2	171.5	25.3	118	10	US-09-918-508-8
3	150	22.1	622	10	US-09-801-368-328
4	146	21.5	1018	15	US-10-101-464A-909
5	145	21.4	1220	10	US-09-801-368-332
6	143.5	21.2	712	10	US-09-801-368-366
7	137.5	20.3	974	15	US-10-126-120-2
8	137	20.2	125	10	US-09-918-508-7
9	132	19.5	1829	15	US-10-156-761-10049
10	128	18.9	1081	10	US-09-424-951-4
11	127.5	18.8	2150	14	US-10-135-322-17
12	126.5	18.7	227	9	US-09-815-242-1131
13	126	18.6	203	15	US-10-156-761-12532
14	125.5	18.5	227	15	US-10-156-761-9975
15	124.5	18.4	232	9	US-09-815-242-13783

16	124	18.3	971	14	US-10-116-048-2	Sequence 2, Appli
17	124	18.3	2471	14	US-10-116-048-4	Sequence 4, Appli
18	123.5	18.2	185	11	US-09-769-787-54	Sequence 54, Appli
19	123	18.1	1447	15	US-10-156-761-8624	Sequence 8624, Ap
20	122.5	18.1	248	15	US-10-156-761-12602	Sequence 12602, A
21	122.5	18.1	1044	15	US-10-101-464A-956	Sequence 956, App
22	122	18.0	248	9	US-09-815-242-12098	Sequence 12098, A
23	121.5	17.9	218	15	US-10-156-761-13746	Sequence 13746, A
24	120.5	17.8	222	9	US-09-815-242-11629	Sequence 11629, A
25	118.5	17.5	232	9	US-09-815-242-10420	Sequence 10420, A
26	118	17.4	890	15	US-10-101-464A-958	Sequence 958, App
27	118	17.4	1270	15	US-10-101-464A-979	Sequence 979, App
28	117.5	17.3	1173	14	US-10-135-322-19	Sequence 19, Appli
29	117.5	17.3	1176	10	US-09-918-508-2	Sequence 2, Appli
30	117	17.3	1383	15	US-10-156-761-13096	Sequence 13096, A
31	115	17.0	762	15	US-10-101-464A-114	Sequence 114, App
32	114.5	16.9	243	15	US-10-156-761-11581	Sequence 11581, A
33	113	16.7	747	12	US-10-100-294A-27	Sequence 27, Appli
34	113	16.5	228	15	US-10-156-761-10048	Sequence 10048, A
35	111.5	16.4	235	10	US-09-738-626-6370	Sequence 6370, Ap
36	111	16.4	669	11	US-09-819-142-24	Sequence 24, Appli
37	111	16.4	1036	10	US-09-918-508-4	Sequence 4, Appli
38	110.5	16.3	104	14	US-10-135-322-30	Sequence 30, Appli
39	110	16.2	573	11	US-09-819-142-10	Sequence 10, Appli
40	110	16.2	599	15	US-10-101-464A-117	Sequence 117, App
41	110	16.2	816	15	US-10-101-464A-827	Sequence 827, App
42	110	16.2	1240	15	US-10-101-464A-976	Sequence 976, App
43	109.5	16.2	100	14	US-10-135-322-29	Sequence 29, Appli
44	109.5	16.2	1092	14	US-10-135-322-18	Sequence 18, Appli
45	107	15.8	197	15	US-10-156-761-10458	Sequence 10458, A

ALIGNMENTS

RESULT 1
US-10-101-464A-127
Sequence 127, Application US/10101464A
Publication No. US20030046728A1
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: And Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020C2
CURRENT APPLICATION NUMBER: US/101.464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO 127
LENGTH: 261
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-127

Query Match 29.8%; Score 202; DB 15; Length 261;

Best Local Similarity 36.5%; Pred. No. 4.4e-14;

Matches 42; Conservative 34; Mismatches 37; Indels 2; Gaps 2;

QY 18 VLIVDDPLNLIIHKIKKIGGISTQANNGEAVIHRDGGSFLLIMDKEMPERDGV 77

Db 137 ILIVEDTQINRIIFGRVLQSLNLCERANGKAVDYFKQ-GRYDVLVMDKEMPWDGH 195

QY 78 STTKKLREMYKSMIVGVTSLADNEERAPFMEAGLNHCLAKPLTKDKIPLINQ 132

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196 EATQRLSRMGVKTPIVALTA-NTIQSDKDLFFAGVDDFQSQPISRDRLVQLDQ 249
db

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RESULT 2

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US-09-918-508-8
; Sequence 8, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918:508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-918-508-8

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Query Match	25.3%	Score 171.5	DB 10	Length 118
Best Local Similarity	33.9%	Pred. No. 3.2e-11		
Matches	37	Conservative 32	Mismatches 3	Gaps 2

QY	18	VLIVDDPLNLIHETIKAGISQTPANNGEAVTHRDGSSFDLIMDKEMPERDGV	77
DB	6	ILAVDDHPINRLADQLGSLGYQCKTANGVDALNVL--SKNHDIVLSDDVNNPNMDGY	63
QY	78	STTKKLREWEKSMIVGVTSIADNEEBERRAFMEAGLNHCLAKPLTKDKI	126
DB	64	RUTORIROLGTLPVIGVTANALAEKQRC--LESGMDSCLSKFVTLDEVI	111

RESIST 3

US-09-801-368-328
; Sequence 328, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 328
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-328

Query Match	22.1%	Score 150;	DB 10;	Length 622;
Best Local Similarity	28.1%;	Pred. No. 7.3e-08;		
Matches	38;	Conservative 32;	Mismatches 45;	Indels 20; Gaps 4;
12	IKKKNLVLTVDDEPLNLIHBEKIIKAIIGISOTANNGBEAVII--HRDGGSSFDLIIMD	68		
373	LRKGPHLVLEDVAVSIQCSKFLRYGCTQVVVDGSLSTLEKYR-----YDLVIMD	427		
69	KEMPERDGVSTTKCLREMEVSMIVGVTSLADNBEERAFMEAGLNHCLAKPLTKDKI--	126		
428	IYWPNLGDGATATSVIRSPDNETPIIATMGNIW--QDLITYLQHGWNIDILAKFFTRDDLHS	486		
127	-----IPLINQ	132		
487	ILIRYVKDRIPLCEQ	501		

RESULT 4

```

US-10-101-464A-909
; Sequence 909, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/238,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 909
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-909

```

```

Query Match      21.5%; Score 146; DB 15; Length 1018;
Best Local Similarity 25.2%; Pred. No. 4e-07;
Matches         41; Conservative 35; Mismatches 53; Indels 34; Gaps 3
3  TKSWMGIEKIKKLVNLIYDDPLNLITHEKIIKAIGISQTANNGEAAVTHRDGSGSF 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
858 SSSIVEEPKPKPKILLVEDKNINVMVQSMKOLGHSMGVVNNNGVEAV--HAVQQSTY 915
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
63  DLILMDKEMPERDGVSTTKKL-----REMEVKSM 91
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
916 DLILMDVCHVNVNGLQATRIISFPMGNWDAVNAGIELVSSDLSCNGHSRSRESKERV 975
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
92  IVGVTSLADNEERRAFMEAGLNHCLAKPLTKDKTIPLINQM 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
976 IIAMTANALSEGADCECFAN-GMDSFVSKPVTOKLKCQLEOVL 1017
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

पञ्चमः ५

```

RESULT 5
US-09-801-368-332
; Sequence 332, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Bubby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug

```

```
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332

Query Match      21.4%; Score 145; DB 10; Length 1220;
Best Local Similarity 29.0%; Pred. No. 6.6e-07;
Matches 40; Conservative 40; Mismatches 44; Indels 14; Gaps 6;

QY      8 DIEKKKLVNVLVDDPDLNLIHKKIKA---IGGIS--QTANNGBEA---VTHRDGG 59
DB      1080 DDCKNETSVKVLVEDNHVN---QEVKRNLEGIENIELACDQGEAFDKVETSKG 1135
QY      60 SSFDLILMDKEMPDRGVSTTKKL-REMEVKSMIVGVTSIADNEEERRRAMEAGLNHCLA 118
DB      1136 ENYNIWFNDVQMPKVDGLLSTYMTNRDLGYTSPVALTAPADDSNIKEC-LESQMGFLS 1194
QY      119 KPLTKDKIPLINQMDA 136
DB      1195 KPIKRPKLTLTIFCAA 1212

RESULT 6
US-09-801-368-366
; Sequence 366, Application US/09801368
; Patent No. US20020128250Al
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 366
; LENGTH: 712
; TYPE: PRT
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; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-366

Query Match      21.2%; Score 143.5; DB 10; Length 712;
Best Local Similarity 27.9%; Pred. No. 4.5e-07;
Matches 39; Conservative 28; Mismatches 42; Indels 31; Gaps 3;

QY      10 ETKKKLVNVLVDDPDLNLIHKKIKAIGGISQTANNGBEAVIHRDGGSFDLILMDK 69
DB      498 EKVPFKINVLIVEDNVINQILGSLFKHKHSYKLAHQGEAVNIWKEGG--LHLIFMDL 555
QY      70 EMPERDGVSTTKKLREMEVKSS-----MIYGVTSIADN 101
DB      556 QLPVLGIEAAKQIRDFEKQNGIGIQKSLNNSHSLNLEKTSKFPSCAPVLIIVALTASNSQ 615
QY      102 EEERRAPMEAGLNHCLA 121
DB      616 MDKEKALL-SGCNDYLTTPV 634

RESULT 7
US-10-126-120-2
; Sequence 2, Application US/10126120
; Publication No. US20030108526A1
; GENERAL INFORMATION:
; APPLICANT: Takei, Kentaro
; APPLICANT: Sakakibara, Hitoshi
; TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FACTORS
; FILE REFERENCE: 11127-004001
; CURRENT APPLICATION NUMBER: US/10/126,120
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: JP 2001-291059
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Zea mays
US-10-126-120-2

Query Match      20.3%; Score 137.5; DB 15; Length 974;
Best Local Similarity 24.6%; Pred. No. 3.2e-06;
Matches 35; Conservative 32; Mismatches 46; Indels 29; Gaps 3;

QY      17 NVLIVDDPDLNLIHKKIKAIGGISQTANNGBEAVI---HRDGGSFDLILMDKEMP 72
DB      830 NILVVDNKNLKVAAALKKYGANVSCVSGKDAISLLQPPHR-----FDACFMDVQMP 884
QY      73 ERDGVSTTKKLREMEVKSMIVGVTSIADNEEERRA-----FMEAG 112
DB      885 EMDGFATGQIRQMLKANERKNKLASIEGSTTBYHLPVLAMTADVIQATYECIKSG 944
QY      113 LNHCLAKPLTKDKIPLINOLM 134
DB      945 MDGVSKPFDDEQLYQAVSRV 966

RESULT 8
US-09-918-508-7
; Sequence 7, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-918-508-7

Query Match      20.2%; Score 137; DB 10; Length 125;
Best Local Similarity 29.4%; Pred. No. 2.1e-07;
Matches 37; Conservative 38; Mismatches 37; Indels 14; Gaps 6;

QY 16 LNVLIYDDPPLNLIHEKIKA---IGGTS--QTANNGEEA---VLIHRDGGSSFDLILM 67
Db 4 VKLIVVEDNEVN---QEVKMLNLEGHETELACDQGEAFDKVKTSLTSGENTNMLFM 59

QY 68 DKEMPERDGVSTTKGL-REMEVKSMIVGTVSLADNEERRAFMEAGLNHCLAKPLTKDKI 126
Db 60 DVQMPKVDGLSTKMIRDLGTVSPIVALTAFADDSNIKEC-LESCMNGFLSKPIKRPKL 118

QY 127 IPLINQ 132
Db 119 KTIUTE 124

RESULT 9
US-10-156-761-10049
; Sequence 10049, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10049
; LENGTH: 1829
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10049

Query Match      19.5%; Score 132; DB 15; Length 1829;
Best Local Similarity 31.5%; Pred. No. 3.1e-05;
Matches 39; Conservative 24; Mismatches 51; Indels 10; Gaps 4;

QY 18 VLIYDDPPLNLIHEKIKAIGGTSQTANNGEEAVII---HRDGGSSFDLILMDKEMPER 74
Db 1710 VLIYDDIRNVFALTSVLEQHGSLVYAENRGREGIVLEQDHD----VTVVLMNDIMFEM 1765

QY 75 DGVSTTKKLREME--VKSMIVGTVSLADNEERRAFMEAGLNHCLAKPLTKDKIPLINQ 132
Db 1766 DGVATTAIRMPQFAGLPITALTAKAMGDREKA-IESGASDVYTKPVDPPHLLTVMEQ 1824

QY 133 LMDA 136
Db 1825 WURA 1828

RESULT 10
US-09-424-951-4
; Sequence 4, Application US/09424951
; Patent No. US20020137034A1

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; GENERAL INFORMATION:
; APPLICANT: SRIKANTHA, THYAGARAJAN
; APPLICANT: SOLL, DAVID R.
; TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT HYBRID KINASE GENE,
; FILE REFERENCE: 087714/0113, AND USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/424,951
; CURRENT FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: PCT/US98/11658
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,914
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1081
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-424-951-4

Query Match      18.9%; Score 128; DB 10; Length 1081;
Best Local Similarity 28.3%; Pred. No. 4e-05;
Matches 43; Conservative 31; Mismatches 48; Indels 30; Gaps 7;

QY 5 SMGDIEKIKKLNVLIVDDPPLNLIHEKIKAIGGTSQTANNGEEAV-IHRDGGSSFD 63
Db 865 SQNSDESRYK--ILLAEDNLVNQKLAVRILEKQHLVVEVNGLEAYEAIKR---NKYD 919

QY 64 LILMDKEMPERDGVSTTKKLREMEVKS-----MIVGVTS---LADNEERRAFME 110
Db 920 VVIMDVQMPVGMGGFEATEKIQWEKKSNPIDSLTRPTIALTAAHMLGDRKS----LA 975

QY 111 AGLNHLAKPL-----TKDKIPLINQLMD 135
Db 976 KGWDDVSVSKPLKPKLLMQTIKKCIHNINQLKE 1007

RESULT 11
US-10-135-322-17
; Sequence 17, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; LENGTH: 2150
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-17

Query Match      18.8%; Score 127.5; DB 14; Length 2150;
Best Local Similarity 32.5%; Pred. No. 0.00012;
Matches 37; Conservative 20; Mismatches 50; Indels 7; Gaps 3;

QY 13 KKKLNVLIVDDPPLNLIHEKIKAIGGTSQTANNGEEAVIHRDGGSSFDLILMDKEMP 72
Db 2024 RKK--ALIVEDNELNRKVLQKLFKKIDWTISFAENGREA-LKEITGRCFDFVMDCOMP 2080

QY 73 ERDGVSTTK----KLREMEVKSIMVGVTSIADNEERRAFMEAGLNHCLAKPLT 122
Db 2081 VLDGGFQTTKIIRSKERENKWKEMNIVALSGSSSFVQDCLDSGMDSFMGKPI 2134

```

RESULT 12

US-09-815-242-11131
; Sequence 11131, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haseibeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11131
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11131

Query Match 18.7%; Score 126.5; DB 9; Length 227;
Best Local Similarity 29.1%; Pred. No. 6.7e-06;
Matches 34; Conservative 30; Mismatches 46; Indels 5; Gaps 2;

QY 18 VLIVDDPLNLIHEKIIKAIGISQTANNGEAVIHRDGGSSFDLILMDKEMPERGV 77
Db 4 LLLVDDIIEITLLSTLEEGFDVETANNGLAEL---QKLNSTKLVLLDVMPLKNGI 60

QY 78 STTKKLEMEVSKMIVGVTSADNEEERRAFMEAGLNHCLAKPLTKDKIPLINQLM 134
Db 61 ETLKEIR--KVSNPVWMLTARGEDIDRVIGLELGADDCLPKPFNDRELIARIKAIL 115

RESULT 13

US-10-156-761-12532
; Sequence 12532, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9975
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9975

Query Match 18.5%; Score 125.5; DB 15; Length 227;
Best Local Similarity 29.2%; Pred. No. 8.6e-06;
Matches 38; Conservative 28; Mismatches 53; Indels 11; Gaps 5;

QY 10 EKIKKKLVIVDDPLNLIHEKIIKAIG---GIS--QTANNGEAVIHRDGGSSFDL 64
Db 4 EBSRKPAAVWVADD---QTVVREGIVMLLGLPGIEVVGAGDGHEAVKLVAE--LNPDV 58

QY 65 ILMKEMPERDGVSTTKKLEMEVSKMIVGVTSADNEEERRAFMEAGLNHCLAKPLTKD 124
Db 59 VLMDLRMPRCDDVETATRRIRAEHPGTQVVVLTITADDESIFPA--LRAGARGYITKAGGD 117

QY 125 KIPLINQLM 134
Db 118 EIVRAVESVL 127

RESULT 15

US-09-815-242-13783
; Sequence 13783, Application US/09815242

; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12532
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12532

Query Match 18.6%; Score 126; DB 15; Length 203;
Best Local Similarity 29.5%; Pred. No. 6.5e-06;
Matches 36; Conservative 20; Mismatches 46; Indels 20; Gaps 3;

QY 17 NVLIVDDPLNLIHEKIIKAIGISO--TANNGEAVIHRDGGSSFDLILMDKEMPER 74
Db 3 SYLVCDSDSFLAREALRAVATVPGVERTTAANGEE--VLRRWGADESDILMDVMPGL 60

QY 75 DGVSTTKKLEMEVSKMIVGVTSADNEEERRAFMEAGLNHCL 118
Db 61 GGVETVRKLLSADPGARIIMLTVAEDLDGVALAVAGARGYLHKDASRAELRATVITQALA 120

QY 119 KP 120
Db 121 DP 122

RESULT 14

US-10-156-761-9975
; Sequence 9975, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9975
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9975

Query Match 18.5%; Score 125.5; DB 15; Length 227;
Best Local Similarity 29.2%; Pred. No. 8.6e-06;
Matches 38; Conservative 28; Mismatches 53; Indels 11; Gaps 5;

QY 10 EKIKKKLVIVDDPLNLIHEKIIKAIG---GIS--QTANNGEAVIHRDGGSSFDL 64
Db 4 EBSRKPAAVWVADD---QTVVREGIVMLLGLPGIEVVGAGDGHEAVKLVAE--LNPDV 58

QY 65 ILMKEMPERDGVSTTKKLEMEVSKMIVGVTSADNEEERRAFMEAGLNHCLAKPLTKD 124
Db 59 VLMDLRMPRCDDVETATRRIRAEHPGTQVVVLTITADDESIFPA--LRAGARGYITKAGGD 117

QY 125 KIPLINQLM 134
Db 118 EIVRAVESVL 127

RESULT 15

US-09-815-242-13783
; Sequence 13783, Application US/09815242

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	202	29.8	261	4	US-09-228-986-127	Sequence 127, App
2	152.5	22.5	946	4	US-09-228-352-7973	Sequence 7973, App
3	150	22.1	1014	4	US-09-252-991A-13138	Sequence 13138, A
4	148	21.8	947	4	US-09-252-991A-29359	Sequence 29359, A
5	147	21.7	1627	4	US-09-252-991A-20395	Sequence 20395, A
6	145	21.4	1220	2	US-08-843-530B-36	Sequence 36, Appl
7	144	21.2	162	4	US-09-252-991A-17557	Sequence 17557, A
8	139.5	20.6	1281	2	US-08-843-530B-6	Sequence 6, Appl
9	139.5	20.6	1298	2	US-08-843-530B-2	Sequence 2, Appl
10	139.5	20.6	1298	2	US-08-843-530B-4	Sequence 4, Appl
11	139.5	20.6	1298	2	US-08-843-530B-34	Sequence 34, Appl
12	139.5	20.6	1441	4	US-09-252-991A-28143	Sequence 28143, A
13	138.5	20.4	234	4	US-09-634-238-220	Sequence 220, App
14	135.5	20.0	760	4	US-09-252-991A-25928	Sequence 25928, A
15	135.5	20.0	860	4	US-09-252-991A-26112	Sequence 26112, A
16	133.5	19.7	938	2	US-08-843-530B-35	Sequence 35, Appl
17	131	19.3	764	4	US-09-252-991A-18607	Sequence 18607, A
18	131	19.3	1036	4	US-09-252-991A-27075	Sequence 27075, A
19	130	19.2	1081	2	US-08-843-530B-18	Sequence 18, Appl
20	130	19.2	1117	2	US-08-843-530B-33	Sequence 33, Appl
21	127	18.7	506	4	US-09-252-991A-18168	Sequence 18168, A
22	125	18.4	227	4	US-09-107-532A-6769	Sequence 6769, Ap
23	124.5	18.4	133	4	US-09-328-352-5134	Sequence 5134, Ap
24	124	18.3	971	3	US-09-112-450-2	Sequence 2, Appl
25	124	18.3	971	4	US-09-419-291A-2	Sequence 2, Appl
26	124	18.3	2471	3	US-09-112-450-4	Sequence 4, Appl
27	124	18.3	2471	4	US-09-419-291A-4	Sequence 4, Appl


```
Query Match      22.5%; Score 152.5; DB 4; Length 946;
Best Local Similarity 30.2%; Pred. No. 3.4e-09;
Matches 39; Conservative 34; Mismatches 41; Indels 15; Gaps 4;

QY 16 LNVIVDDPPLNLIIEHKIKKIGGISTQANNGEAVIHRDGGSS----FDLIIMDKEM 71
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 674 LHILAVDDHPLNVLVLEALLGELANVTKTKALSGQALNIQSRIDQKLPDFLVMFIQM 733
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 72 PERDGVSTTKKLEEM-----EVKSMIVGVT--SLADNEEERRAFMEAGLNHCLAKPLTK 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 734 FVMSGIDTTRAIRSLSTLDGEMQLPIIATAHALAD---EQKLLKVGMDYVTKPIQM 790
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 124 DKIIPLINQ 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 791 EQIIQLITQ 799
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
US-09-252-991A-31338
; Sequence 31338, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31338
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31338

Query Match      22.1%; Score 150; DB 4; Length 1014;
Best Local Similarity 25.5%; Pred. No. 7.4e-09;
Matches 35; Conservative 36; Mismatches 56; Indels 10; Gaps 4;

QY 2 ATKSMGDIKIK--KKNLVIVDDPPLNLIIEHKIKKIGGISTQANNGEAVIHRDGG 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 868 ARSGVAEVEERKARALSILLADHPNRLITLMQLESIGHRVSTEDGEAA--FERWQ 925
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 60 SSFDLIIMDKEMPERDGVSTTKKLEMEV-----KSMIVGVTSLADNEEERRAFMEAGLN 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 926 EDFDVITDGMFRMDGYELARRISQEALGGRRCRLVIALTASAEKDALERC-LAAGWD 984
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 HCLAKPLTKDKIIPLIN 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 985 RVLFKPTTLDELALN 1001
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
US-09-252-991A-29359
; Sequence 29359, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
```

```
; SEQ ID NO 29359
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29359

Query Match      21.8%; Score 148; DB 4; Length 947;
Best Local Similarity 28.8%; Pred. No. 1.1e-08;
Matches 34; Conservative 33; Mismatches 43; Indels 8; Gaps 4;

QY 18 VLIIVDDPPLNLIIEHKIKKIGGISTQANNGEAV-IHRDGGSSFDLIIMDKEMPERDG 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 689 LLCVDNPNANLLVQTLSDLGAVTAVDVSGYAALEVYQRE---RFDLVFMDVQMPQMDG 745
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 77 VSTTKKLEMEVKSMI--VGVTSLADN--EEERRAFMEAGLNHCLAKPLTKDKIIPLI 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 746 RQATEAIRWEAREVSPVPVIALTAHALSNEKALLQAGMDDVLTTPIDEQQLAQVV 803
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-252-991A-20395
; Sequence 20395, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20395
; LENGTH: 1627
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20395

Query Match      21.7%; Score 147; DB 4; Length 1627;
Best Local Similarity 31.9%; Pred. No. 3.3e-08;
Matches 37; Conservative 26; Mismatches 45; Indels 8; Gaps 3;

QY 14 KKNLVIVDDPPLNLIIEHKIKKIGGISTQANNGEAVIHRDGGSSFDLIIMDKEMPE 73
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1371 RLQVLVDDHVNQILHQQLSFLGHVDEAEAGLSALNLWH--GQFFDVITDCHMPL 1428
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 74 RDGVSTTKKLEMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKD 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1429 MSGSGLARSIRQEREENGEPVVIIGLTADAQPEIERC-IOAGNECLIKPIGLD 1483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-08-843-530B-36
; Sequence 36, Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude
; APPLICANT: Agnan, Jacqueline
; APPLICANT: Alex, Lisa A.
; APPLICANT: Simon, Melvin I.
; TITLE OF INVENTION: Osmosensing Histidine Kinases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
```

DB 95 EATLIRREERAQGWPRVPIVTAHILD--EHRRAGIEAGNDAYLQKPVDRALYATLE 152

QY 132 QLM 134

DB 153 RLL 155

RESULT 8

US-08-843-530B-6

; Sequence 6, Application US/08843530B

; Patent No. 5939306

; GENERAL INFORMATION:

; APPLICANT: Selitrennikoff, Claude

; APPLICANT: Agnan, Jacqueline

; APPLICANT: Alex, Lisa A.

; APPLICANT: Simon, Melvin I.

; TITLE OF INVENTION: Osmosensing Histidine Kinases

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/843,530B

; FILING DATE: 16-APR-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MacKnight, Karin T.

; REGISTRATION NUMBER: 38,230

; REFERENCE/DOCKET NUMBER: UTC-02717

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1281 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-843-530B-6

Query Match 20.6%; Score 139.5; DB 2; Length 1281;

Best Local Similarity 31.1%; Pred. No. 1.8e-07;

Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps 5;

QY 2 ATKSMGDIETKIKKLNVLIVDDPLNLIIEHKIIEKIKGIGISQTANNGEAV-IHHRDGS 60

DB 1075 ATPSLAD--NTKSFELLAEADNTVQNLAVKILEYHHVTVVVGNGEAVEAVKR---K 1128

QY 61 SPDLILMKEMPERDGVSTTKKUREME-----VKSMIVGVTSIADNEERAFMEAGLNH 115

DB 1129 KFDVILMDVQPMGPGFEATAKIREYERSLGSGRTPIALTAAH-MMGDRKCIQAQOMDE 1187

QY 116 CLAKPLTKDKIPLI 130

DB 1188 YLSKPLQNHILQTI 1202

RESULT 9

US-08-843-530B-2

; Sequence 2, Application US/08843530B

; Patent No. 5939306

; GENERAL INFORMATION:

; APPLICANT: Selitrennikoff, Claude

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/843,530B

FILING DATE: 16-APR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Karin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: UTC-02717

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 1220 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

US-08-843-530B-36

Query Match 21.4%; Score 145; DB 2; Length 1220;

Best Local Similarity 29.0%; Pred. No. 3.8e-08;

Matches 40; Conservative 40; Mismatches 44; Indels 14; Gaps 6;

QY 8 DIEKIKKLNVLIVDDPLNLIIEHKIIEKIGIS--QTANNGEAV---VLIHRDGG 59

DB 1080 DDDKNTSKVILVDDNHN---QEVIKRLNLEGIEIACDQGAFAKVKELTSKG 1135

QY 60 SSPDLILMKEMPERDGVSTTKKL-REMEVKSMIVGVTSIADNEERAFMEAGLNHCLA 118

DB 1136 ENYMFIMFQVQPKVDGLSTKWRDLGYTSPIVALTAFADDSNIKEC-LESGWNGFLS 1194

QY 119 KPLTKDKIPLNLMDA 136

DB 1195 KPIKPKLTKILTEFCAA 1212

RESULT 7

US-09-252-991A-17557

; Sequence 17557, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 17557

; LENGTH: 162

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-17557

Query Match 21.2%; Score 144; DB 4; Length 162;

Best Local Similarity 30.9%; Pred. No. 2.6e-09;

Matches 38; Conservative 28; Mismatches 49; Indels 8; Gaps 3;

QY 18 VLIVDDPLNLIIEHKIIEKIGISQTANNGEAVIHRDGSFPLILMKEMPERDGV 77

DB 35 ILVAEDNPVNLVVRGFLAKRGVAVRLAGNRLALDEYLRDENGILMDGEMPEMDGF 94

QY 78 STTKUREME-----VKSMIVGVTSIADNEERAFMEAGLNHCLAKPLTKDKIPLIN 131

APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-843-530B-2

Query Match 20.6%; Score 139.5; DB 2; Length 1298;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps 5;

QY 2 ATKSMGDIKIKKLNVLIVDDPLNLIHKKIKAIGGISQTANNGBEAV-IHHRDGS 60
DB 1075 ATPSLAD---NTKSFELLAEADNTVNQLAVKILEKHYHVVTVVVGNGEEAVEAVKR---K 1128

QY 61 SFDLILMDKEMPERDGVSTTKKLEME-----VKSMIVGVTSIADNEEERAFMEAGLNH 115
DB 1129 KFDVILMDVQPMINGGFETAKIRYERSLSGRTPIIALTAHA-MMGDRKCKICQAOQDE 1187

QY 116 CLAKPLTKDKIPI 130
DB 1188 YLSKPLQONHLIQT 1202

RESULT 10
US-08-843-530B-4
Sequence 4, Application US/08843530B
Patent No. 5939306
GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-843-530B-4

Query Match 20.6%; Score 139.5; DB 2; Length 1298;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps 5;

QY 2 ATKSMGDIKIKKLNVLIVDDPLNLIHKKIKAIGGISQTANNGBEAV-IHHRDGS 60
DB 1075 ATPSLAD---NTKSFELLAEADNTVNQLAVKILEKHYHVVTVVVGNGEEAVEAVKR---K 1128

QY 61 SFDLILMDKEMPERDGVSTTKKLEME-----VKSMIVGVTSIADNEEERAFMEAGLNH 115
DB 1129 KFDVILMDVQPMINGGFETAKIRYERSLSGRTPIIALTAHA-MMGDRKCKICQAOQDE 1187

QY 116 CLAKPLTKDKIPI 130
DB 1188 YLSKPLQONHLIQT 1202

RESULT 11
US-08-843-530B-4
Sequence 34, Application US/08843530B
Patent No. 5939306
GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1298 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-843-530B-34

Query Match      20.6%; Score 139.5; DB 2; Length 1298;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps 5;

QY 2 ATKSMGDIKKKLVNVLVDDPDLNLIHEKIIKAIGISQTANNNGEEAV-IHRRGGS 60
DB 1075 ATPSLAD---NTKSPFILLAEADNTQRLAVKILEKHYHVVTVVNGEEAVEAYKR---K 1128
QY 61 SFDLIIMDKEMPERDQVSTTKKLREME-----VKSMIVGVTSADNEERRAFMEAGLNH 115
DB 1129 KFDVILMDVQMPIMGFEATKIREVERSLGSGRTPIIALTAHA-MXGDREKCIQAQWDE 1187
QY 116 CLAKPLTKKIPLI 130
DB 1188 YLSKPLQONHLIQT 1202

RESULT 12
US-09-252-991A-28143
; Sequence 28143, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28143
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-28143

Query Match      20.6%; Score 139.5; DB 4; Length 1441;
Best Local Similarity 28.8%; Pred. No. 2.2e-07;
Matches 34; Conservative 30; Mismatches 43; Indels 11; Gaps 3;

QY 16 LNVLIIVDDPDLNLIHEKIIKAIGISQTANNNGEEAVIIHRRGGSFDLILMDKEMPERD 75
DB 1182 VRLIIVEDNALNRQVAELLSSEGARVALDGLAGVQVLEASVPFDVAVLMDQMCPDID 1241
QY 76 GVSTTKLRE-----NEVKSNIIVGVTSADNEERRAFMEAGLNHCLAKPLTKKII 127
DB 1242 GLEATRRIRADGRFAGLPILANTAN-ASLAD----REACLAAGMNDHVAKPIDKERLV 1294

RESULT 13
US-09-634-238-220
; Sequence 220, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James

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; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043UI
; CURRENT APPLICATION NUMBER: US/09/634,238
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
; US-09-634-238-220

Query Match      20.4%; Score 138.5; DB 4; Length 234;
Best Local Similarity 30.2%; Pred. No. 2e-08;
Matches 35; Conservative 31; Mismatches 47; Indels 3; Gaps 2;

QY 18 VLIIVDDPDLNLIHEKIIKAIGISQTANNNGEEAVIIHRRGGSFDLILMDKEMPERDGV 77
DB 4 ILIVDEFAILLTLQYNLEAEHYQVETADQGEA--LDKVRSEPFDFIILDLMLPSLSGL 61
QY 78 STTKKLREMEVKSMIVGVTSADNEERRAFMEAGLNHCLAKPLTKDKIPLINQL 133
DB 62 DVTCKIREKIQTPIMLTA-KDNETDKIVGLGADDDVTKPSPREIARIKAI 116

RESULT 14
US-09-252-991A-25928
; Sequence 25928, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25928
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-25928

Query Match      20.0%; Score 135.5; DB 4; Length 760;
Best Local Similarity 28.0%; Pred. No. 2.5e-07;
Matches 35; Conservative 31; Mismatches 54; Indels 5; Gaps 3;

QY 4 KSMGDIKKKLVNVLVDDPDLNLIHEKIIKAIGISQTANNNGEEAVIIHRRGGSFSD 63
DB 612 QAAGDAAPVAAGQEILLVEDNPNVQTVIEMLSLGYRVLVADGIQAV--RSAERQRYD 669
QY 64 LILMDKEMPERDQVSTTKKLREMEVKSMIVGVTSADNEERRAFMEAGLNHCLAKPL 121
DB 670 AILMDCLPLVDGYSATREIRAQ-NGRQVPIIALTANALQDRENCIQAQMNDYLAKPF 728
QY 122 TKDKI 126
DB 729 KRAEL 733

RESULT 15
US-09-252-991A-26112
; Sequence 26112, Application US/09252991A

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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26112
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26112

Query Match 20.0%; Score 135.5; DB 4; Length 860;
Best Local Similarity 26.5%; Pred. No. 3e-07;
Matches 36; Conservative 35; Mismatches 56; Indels 9; Gaps 3;
Qy 1 MATKSMGDIKKKLNVLIVDDPLNLIHKKIKAIGGISCTANNGEEAVIIHRDGS 60
Db 722 IAFSSASDTTGEQRNTRVLVEDNPNQLVAKGLLHKLCQVWIAEHGLNALKMLEE--H 779
Qy 61 SFDLILMDKEMPERDGVSTTKKLRM----EVKSMIVGVTSLADNEEERRAFMEAGLNHC 116
Db 780 PIDLVLMDCNNPVMGDGYEATRQIRDSGRWGGLPIIALTANALPDERERCRA---AGMDDY 836
Qy 117 LAKPLTKDKLIPLINQ 132
Db 837 LAKFFHDEKAILDR 852

Search completed: August 14, 2003, 16:51:53
Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 16:46:47 ; Search time 83 Seconds
(without alignments)
260.082 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678
Sequence: 1 MATKMGDIEIKKLNLI.....LAKPLTKDKIPLINQLMDA 136

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	678	100.0	136	20	AA1981.DAT.*
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4	538	79.4	142	21	AA1983.DAT.*
5	515	76.0	142	21	AA1984.DAT.*
6	472	69.6	116	20	AA1985.DAT.*
7	437	64.5	104	21	AA1986.DAT.*
8	437	64.5	104	21	AA1987.DAT.*
9	301	44.4	70	21	AA1988.DAT.*

10	280	41.3	66	21	AAG21090	Arabidopsis thalia
11	213	31.4	71	21	AAG21088	Arabidopsis thalia
12	192.5	29.8	261	21	AA1985159	Pinus radiata cell
13	192.5	28.4	67	20	AA1985159	Brassica napus D22
14	171.5	25.3	118	23	ABG70785	E. coli RscC recel
15	156.5	23.1	471	24	AAO26983	Pseudomonas aerugi
16	156.5	23.1	496	24	AAO26995	Pseudomonas aerugi
17	156.5	23.1	666	24	AAO26994	Pseudomonas aerugi
18	156.5	23.1	709	24	AAO26993	Pseudomonas aerugi
19	156.5	23.1	719	24	AAO26992	Pseudomonas aerugi
20	156.5	23.1	802	24	AAO26991	Pseudomonas aerugi
21	156.5	23.1	870	24	AAO26990	Pseudomonas aerugi
22	156.5	23.1	874	24	AAO26989	Pseudomonas aerugi
23	156.5	23.1	887	24	AAO26988	Pseudomonas aerugi
24	156.5	23.1	900	24	AAO26987	Pseudomonas aerugi
25	156.5	23.1	906	24	AAO26986	Pseudomonas aerugi
26	156.5	23.1	931	24	AAO26985	Pseudomonas aerugi
27	155	22.9	922	22	AA1983276	Histidine protein k
28	149	22.0	1373	23	ABP73292	Candida albicans e
29	148.5	21.9	922	23	ABP73274	Histidine protein k
30	148.5	21.9	922	22	AA1983275	Histidine protein k
31	148.5	21.9	950	23	AB1983422	Herbicidally activ
32	146	21.5	1018	21	AA1985534	Eucalyptus grandis
33	141	20.8	1146	20	AA1986007	Histidine kinase C
34	139.5	20.6	1281	20	AA198484	osl histidine kina
35	139.5	20.6	1298	19	AA1985822	N. crassa osp pro
36	139.5	20.6	1298	20	AA198481	osl-p amino acid s
37	139.5	20.6	1298	20	AA198483	osl histidine kina
38	137	20.2	125	23	ABG70784	Yeast SLN1 receive
39	134.5	19.8	1122	23	AB1982150	Herbicidally activ
40	134	19.8	120	22	AA1986490	Putative P. abyssi
41	133.5	19.7	1023	22	AB1986668	Novel human diago
42	131	19.3	136	23	AB1981215	Human kinase-like
43	131	19.3	674	21	AA1981922	Candida albicans S
44	130	19.2	1081	20	AA198482	osl histidine ki
45	130	19.2	1081	20	AA1981600	Candida albicans C

ALIGNMENTS

RESULT 1

AA19842637
ID AAY42637 standard; Protein; 136 AA.

AC AAY42637;

XX 10-JAN-2000 (first entry)

XX Brassica response regulator protein D22.

XX Signal transduction protein; dehiscence; male sterile plant; D22 gene;
shatter resistance; oilseed rape; response regulator protein.

OS Brassica napus.

XX WO9949046-A1.

XX 30-SEP-1999.

XX 22-MAR-1999; 99WO-GB00905.

XX 20-MAR-1998; 98GB-0006113.

XX (BIOG-) BIOGENMA UK LTD.

XX Wyatt P, Roberts JA, Whitelaw C;

XX WPI; 1999-580449/49.

XX N-PSDB; AA22974.

XX A nucleic acid encoding a signal transduction protein involved in plant

dehiscence, useful for producing shatter resistant male sterile plants

CC sequence represents the B. napus DZ2 putative peptide sequence.

XX
SQ Sequence 136 AA;

Query Match 100.0%; Score 678; DB 20; Length 136;
Best Local Similarity 100.0%; Pred. No. 1e-67;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATKSMGDIKKKKLNVLIVDDDFLNLIIEHKIIKAIGGISQTANNGEAEVVIHRDGG 60
DB 1 MATKSMGDIKKKKLNVLIVDDDFLNLIIEHKIIKAIGGISQTANNGEAEVVIHRDGG 60

QY 61 SFDLILMDKEMPERDGVSTTKKLRMEVKSIMVGVTSIADNEEBERRAFMEAGLNHCLAKP 120
DB 61 SFDLILMDKEMPERDGVSTTKKLRMEVKSIMVGVTSIADNEEBERRAFMEAGLNHCLAKP 120

QY 121 LTKDKIPIPLINQLMDA 136
DB 121 LTKDKIPIPLINQLMDA 136

RESULT 3
AAG10549
ID AAG10549 standard; Protein; 142 AA.
XX
AC AAG10549;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8916.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EF1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.

PT
XX
PS Claim 4; Fig 1; 7lpp; English.

XX The invention provides a nucleic acid encoding a signal transduction
XX protein involved in the process of dehiscence. The nucleic acids and
XX proteins are useful for regulating or controlling dehiscence of a pod or
XX an anther in a plant, useful in the production of male sterile plants.
XX The methods, etc. may be used in the production of shatter resistance or
XX shatter-delayed plants such as oilseed rape (Brassica napus). The present
XX sequence represents a B. napus response regulator protein DZ2.

XX
SQ Sequence 136 AA;

Query Match 100.0%; Score 678; DB 20; Length 136;
Best Local Similarity 100.0%; Pred. No. 1e-67;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATKSMGDIKKKKLNVLIVDDDFLNLIIEHKIIKAIGGISQTANNGEAEVVIHRDGG 60
DB 1 MATKSMGDIKKKKLNVLIVDDDFLNLIIEHKIIKAIGGISQTANNGEAEVVIHRDGG 60

QY 61 SFDLILMDKEMPERDGVSTTKKLRMEVKSIMVGVTSIADNEEBERRAFMEAGLNHCLAKP 120
DB 61 SFDLILMDKEMPERDGVSTTKKLRMEVKSIMVGVTSIADNEEBERRAFMEAGLNHCLAKP 120

QY 121 LTKDKIPIPLINQLMDA 136
DB 121 LTKDKIPIPLINQLMDA 136

RESULT 2
AAV42653
ID AAV42653 standard; Protein; 136 AA.
XX
AC AAV42653;
XX
DT 10-JAN-2000 (first entry)
XX
DE Brassica response regulator protein DZ2 putative peptide sequence.
XX
KW Signal transduction protein; dehiscence; male sterile plant; DZ2 gene;
KW shatter resistance; oilseed rape; response regulator protein.
XX
OS Brassica napus.
XX
PN WO9949046-A1.
XX
PD 30-SEP-1999.
XX
PF 22-MAR-1999; 99WO-GB00905.
XX
PR 20-MAR-1998; 98GB-0006113.
XX
PA (BIOG-) BIOGEMMA UK LTD.
XX
PY Wyatt P, Roberts JA, Whitelaw C;
XX
WI: 1999-580449/49.
XX
N-PSDB; AA222977.

PT
XX
PS A nucleic acid encoding a signal transduction protein involved in plant
XX dehiscence, useful for producing shatter resistant male sterile plants

XX
SQ Example 2; Fig 6; 7lpp; English.

XX The invention provides a nucleic acid encoding a signal transduction
XX protein involved in the process of dehiscence. The nucleic acids and
XX proteins are useful for regulating or controlling dehiscence of a pod or
XX an anther in a plant, useful in the production of male sterile plants.
XX The methods, etc. may be used in the production of shatter resistance or
XX shatter-delayed plants such as oilseed rape (Brassica napus). The present
XX sequence represents a B. napus response regulator protein DZ2.

PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 17-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139750.
 PR 21-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140655.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140823.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
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 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 30-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-SEP-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 14-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
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 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.


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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 79.4%; Score 538; DB 21; Length 142;
Best Local Similarity 78.9%; Pred. No. 4.7e-52;
Matches 112; Conservative 8; Mismatches 16; Indels 6; Gaps 2;

QY . 1 MATKMGDIK-----TKKL-NVLIYDDPDLNLIHKKIKAIGGISOTANGGEAVII 54
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MATKSTGGTEKTKSIEYVKKGLINLIYDDPDLNRLHEMIKTIGGISOTAKNGGEAVIL 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 55 HRDGGSPDLILMDKEMPERDGVSTTKKLEMEYKSMIVGVTSIADNEERERAFMEAGIN 114
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 HRDGEASFDLILMDKEMPERDGVSTTKKLEMKVTSWIVGVTSVADQEEERKAFMEAGIN 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 HCLAKPLTKDKIIPILNQLMDA 136
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 HCLEKPLTKAKIPFLISHLFDA 142
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
RAG44439
ID AAG44439 standard; Protein; 142 AA.
XX
AC AAG44439;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55668.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
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PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
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PR 24-MAY-1999; 99US-0135629.
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PR 27-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
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PR 18-JUN-1999; 99US-0139454.
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PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
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PR 24-JUN-1999; 99US-0140695.
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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 09-JUL-1999; 99US-0142803.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
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PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
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XX SQ Sequence 142 AA;
Query Match 76.08; Score 515; DB 20; Length 142;
Best Local Similarity 76.14; Pred. No. 1.7e-49;
Matches 108; Conservative 8; Mismatches 20; Indels 6; Gaps 2;
QY 1 MATKSMGDIK-----IKKEL-NVLIIVDDPLNLIHEKIIKAIGISOTANNGEEAVII 54
DB : 1 MATKSTGTGTEKTSIEVKKKLNVLIVDDPLNRLHEMIKIITIGISQTAKNGEXVIL 60
QY 55 HRDGGSSFDLILMDKXENPERDGVSTTKKLEBMEVKSMIVGVTSIADNNEERRAFWEAGLN 114
DB 61 HRDGEAFDILMDKXENPERDGVSTTKKLEBMEVKSMIVGVTSIADNNEERRAFWEAGLN 120
QY 115 HCLAKPLTKDKIIPILNQLMDA 136
DB 121 HCLEKPLTKAKIPILNQLMDA 142
RESULT 6
AAY42652
ID AAY42652 standard; Protein; 116 AA.
XX
AC AAY42652;
XX
DT 10-JAN-2000 (first entry)
XX
DE Brassica response regulator protein D22B putative peptide sequence.
XX
KW Signal transduction protein; dehiscence; male sterile plant; D22B gene;
KW shatter resistance; oilseed rape; response regulator protein.
XX
OS Brassica napus.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "unknown"
FT
XX
XX WO9949046-A1.
XX
XX 30-SEP-1999.
XX
XX 22-MAR-1999; 99WO-GB00905.
XX
XX 20-MAR-1998; 98GB-0006113.
XX
XX (BIOG-) BIOGEMMA UK LTD.
XX
XX Wyatt P, Roberts JA, Whitelaw C;
XX
XX WPI; 1999-580449/49.
XX
XX N-PSDB; AAZ22976.
XX
XX A nucleic acid encoding a signal transduction protein involved in plant
XX dehiscence, useful for producing shatter resistant male sterile plants
XX
XX Example 2; Fig 6; 71pp; English.
XX
XX The invention provides a nucleic acid encoding a signal transduction
XX protein involved in the process of dehiscence. The nucleic acids and
XX proteins are useful for regulating or controlling dehiscence of a pod or
XX an anther in a plant, useful in the production of male sterile plants.
XX The methods, etc. may be used in production of shatter resistance or
XX shatter-delayed plants such as oilseed rape (Brassica napus). The present
XX sequence represents the B. napus D22B putative peptide sequence.
XX
SQ Sequence 116 AA;
Query Match 69.68; Score 472; DB 20; Length 116;
Best Local Similarity 80.24; Pred. No. 8.4e-45;
Matches 93; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 21 VDDPLNLIHEKIIKAIGISOTANNGEEAVIIHRDGGSSFDLILMDKXENPERDGVSTT 80
DB 1 VDDPVIKRLHEIIKISGISQTAKNGEEAVIIHRDGNASFDLILMDKXENPERDGLSAT 60
QY 81 KCLREMEVKSMIVGVTSIADNNEERRAFWEAGLNHCLAKPLTKDKIIPILNQLMDA 136
DB 61 KCLREMKVTSIIGVTTIADNNEERRAFWEAGLNHCLAKPLSKAKIIPILNQLMDA 116
RESULT 7
AAG10550
ID AAG10550 standard; Protein; 104 AA.
XX
AC AAG10550;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8917.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0130891.
XX 30-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
XX 07-MAY-1999; 99US-0132863.
XX 11-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.
XX 14-MAY-1999; 99US-0134221.
XX 14-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134768.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.
XX 21-MAY-1999; 99US-0135353.
XX 24-MAY-1999; 99US-0135629.
XX 25-MAY-1999; 99US-0136021.
XX 27-MAY-1999; 99US-0136392.
XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137528.
XX 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
XX 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.

Db 2 IIKTIGGISQAKNGEEAVILHRDGEASFDLILMDKEMPERDGVSTTKKLEMKVTSMIV 61

Qy 94 GVTSLADNEEERRRFRWAGLNHCLAKPLTKDKIPLINOLMDA 136

Db 62 GVTSLADNEEERRRFRWAGLNHCLAKPLTKDKIPLINOLMDA 104

RESULT 8

AAAG44440

ID -AAG44440 standard; Protein; 104 AA.

AC AAG44440;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 55669.

KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

PN 06-SEP-2000.

XX 25-FEB-2000; 2000EP-030439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 23-MAR-1999; 99US-0126264.

PR 23-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 16-APR-1999; 99US-0128714.

PR 19-APR-1999; 99US-0129645.

PR 21-APR-1999; 99US-0130049.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

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DT 17-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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OS Arabidopsis thaliana.
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QY 127 IPLINQLMDA 136
 Db 61 FPLISHLFDA 70

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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 23519.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
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PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
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PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 09-AUG-1999; 99US-0148171.
PR 10-AUG-1999; 99US-0148319.
PR 11-AUG-1999; 99US-0148341.
PR 12-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 13-AUG-1999; 99US-0149368.
PR 16-AUG-1999; 99US-0149175.
PR 17-AUG-1999; 99US-0149426.
PR 18-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149722.

PR	20-AUG-1999;	99US-0149723.	ID	AG21088 standard; Protein; 71 AA.
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PR	23-AUG-1999;	99US-0149902.	AC	AG21088;
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PR	26-AUG-1999;	99US-0150884.	XX	
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PR	27-AUG-1999;	99US-0151066.	XX	
PR	27-AUG-1999;	99US-0151080.	XX	Protein identification; signal transduction pathway; metabolic pathway;
PR	30-AUG-1999;	99US-0151080.	KW	hybridisation assay; genetic mapping; gene expression control; promoter;
PR	31-AUG-1999;	99US-0151438.	KW	termination sequence.
PR	01-SEP-1999;	99US-0151930.	XX	
PR	07-SEP-1999;	99US-0152363.	OS	Arabidopsis thaliana.
PR	10-SEP-1999;	99US-0153070.	XX	
PR	13-SEP-1999;	99US-0153758.	PN	EP1033405-A2.
PR	15-SEP-1999;	99US-0154018.	XX	
PR	16-SEP-1999;	99US-0154039.	PD	06-SEP-2000.
PR	20-SEP-1999;	99US-0154779.	XX	
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PR	06-OCT-1999;	99US-0157865.	PR	29-MAR-1999; 99US-0126785.
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PR	13-OCT-1999;	99US-0159294.	PR	19-APR-1999; 99US-0130077.
PR	13-OCT-1999;	99US-0159295.	PR	21-APR-1999; 99US-0130449.
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PR	18-OCT-1999;	99US-0159584.	PR	05-MAY-1999; 99US-0132485.
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PR	21-OCT-1999;	99US-0160815.	PR	14-MAY-1999; 99US-0134218.
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PR	26-OCT-1999;	99US-0161361.	PR	27-MAY-1999; 99US-0136392.
PR	28-OCT-1999;	99US-0161920.	PR	28-MAY-1999; 99US-0136782.
PR	28-OCT-1999;	99US-0161992.	PR	01-JUN-1999; 99US-0137222.
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PR	28-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139458.
PR	28-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139459.
PR	28-OCT-1999;	99US-0162142.	PR	18-JUN-1999; 99US-0139460.

Query Match 41.3%; Score 280; DB 21; Length 66;
Best Local Similarity 84.8%; Pred. No. 1.1e-23;
Matches 56; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 71 MPERDGVSTTKLRENEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKPLTKDKIPLI 130
Db 1 MPERDGVSTTKLRENEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKPLTKDKIPLI 60
Qy 131 NOLMDA 136
Db 61 SHLFDA 66

RESULT 11
AAG21088


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XX DT 27-NOV-2000 (first entry)
XX DE Pinus radiata cell signalling involved protein SEQ ID NO:127.
XX KW Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
XX KW plant cell signalling; modulation; transgenic plant; pathogen; growth;
XX KW environmental change; development; cell proliferation; differentiation;
XX KW elongation; survival; disease resistance; nutrient metabolism.
XX OS Pinus radiata.
XX PN WO200042171-A1.
XX PD 20-JUL-2000.
XX PF 11-JAN-2000; 2000WO-US00724.
XX PR 12-JAN-1999; 99US-0228986.
XX PR 01-NOV-1999; 99US-0162866.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX Strabala TJ, Nieuwenhuizen NJ;
XX WPI; 2000-476052/41.
XX Isolated polynucleotide encoding a polypeptide involved in cell
XX signaling used for generating transgenic plants with modified responses
XX to external signals.
XX Claim 3; Page 104-105; 527pp; English.
XX AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
XX and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
XX pine (Pinus radiata) also known as Monterey pine). The protein sequences
XX are involved in cell signalling. The polynucleotide and protein
XX sequences can be used to modify the response of plant cells to external
XX signals e.g. environmental changes or pathogens during the growth and
XX development of a plant. They can be used to modify cell proliferation,
XX differentiation, elongation and survival, resistance to disease and
XX nutrient metabolism. Examples of modifications which can be produced are
XX altered fruit ripening and senescence of leaves and flowers e.g. to
XX delay senescence and prolong the life of cut flowers or enhance
XX senescence of reproductive organs to engineer sterile plants. Other
XX modifications can be used to delay senescence in selected cell types or
XX organs providing fruit and vegetables which have a longer shelf life
XX between harvest and consumption, or to decrease branching frequency in
XX forest tree species giving long stretches of valuable knot-free clear
XX wood which can be used in solid timber furniture and veneers.
XX SQ Sequence 261 AA;
Query Match 29.8%; Score 202; DB 21; Length 261;
Best Local Similarity 36.5%; Pred. No. 3.7e-14;
Matches 42; Conservative 34; Mismatches 37; Indels 2; Gaps 2;
QY 18 VLIVDDPLNLIHKKIKATGISTANNGEEAVIHRDGGSSFDILMDKMPREDGV 77
DB 137 ILLVEDTQINRIIFGRVLQSLNLYCEEAEKGVADVFKQ-GRTYDVLVMDKMPVNDGH 195
QY 78 STTKLREMEVKSMTVGVTSIADNEEEERAFWEAGLNHCLAKPLTKDKIPLINQ 132
DB 196 EATRLQSRGVKTPIVALTA-NLQSDKDLFFEAGVDDFQSKPLSRDLVQLLDQ 249
RESULT 13
AAY42644
ID AAY42644 standard; Protein; 67 AA.
XX AC AAY42644;
XX DT 10-JAN-2000 (first entry)

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XX DE Brassica napus DZ2B partial fragment.
XX KW Signal transduction protein; dehiscence; male sterile plant; DZ2B gene;
XX KW shatter resistance; oilseed rape; response regulator protein.
XX OS Brassica napus.
XX PN WO9949046-A1.
XX PD 30-SEP-1999.
XX PF 22-MAR-1999; 99WO-GE00905.
XX PR 20-MAR-1998; 98GB-0006113.
XX PA (BIOG-) BIOGENMA UK LTD.
XX Wyatt P, Roberts JA, Whitelaw C;
XX WPI; 1999-580449/49.
XX DR N-FSDS; AAZ22975.
XX A nucleic acid encoding a signal transduction protein involved in plant
XX dehiscence, useful for producing shatter resistant male sterile plants
XX Example 2; Fig 5; 71pp; English.
XX The invention provides a nucleic acid encoding a signal transduction
XX protein involved in the process of dehiscence. The nucleic acids and
XX proteins are useful for regulating or controlling dehiscence of a pod or
XX an anther in a plant, useful in the production of male sterile plants.
XX The methods, etc. may be used in the production of shatter resistance or
XX shatter-delayed plants such as oilseed rape (Brassica napus). The present
XX sequence represents the partial fragment of B. napus DZ2B protein.
XX SQ Sequence 67 AA;
Query Match 28.4%; Score 192.5; DB 20; Length 67;
Best Local Similarity 65.7%; Pred. No. 6.7e-14;
Matches 44; Conservative 6; Mismatches 10; Indels 7; Gaps 2;
QY 1 MAT--KSMGDIK-----IKKLNVLIVDDPLNLIHKKIKATGISTANNGEEAVI 53
DB 1 MATSTGTGDIKTKSVKVKLNVLIVDDTIVTKLHNIIRKSIKSGISQTAKNGEEAVN 60
QY 54 IHRDGS 60
DB 61 IHRDGA 67
RESULT 14
ABG70785
ID ABG70785 standard; Protein; 118 AA.
XX AC ABG70785;
XX DT 09-DEC-2002 (first entry)
XX B. coli RscC receiver region of histidine kinase.
XX RscC; antagonist; agonist; cytokinin receptor;
XX KW receptor; signal transduction; histidine kinase; hormone; cell division;
XX KW cell differentiation; agriculture; growth regulator; harvest.
XX OS Escherichia coli.
XX PN EP1241182-A2.
XX PD 18-SEP-2002.
XX DT 13-MAR-2002; 2002EP-0005749.

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